

PD 04-MAY-2000.
 XX 28-OCT-1999; 99NC-CA00992.
 PF 28-OCT-1998; 98US-0106034.
 XX 28-OCT-1998; 98US-0106039.
 PR 28-OCT-1998; 98US-0106042.
 PR 28-OCT-1998; 98US-0106044.
 PR 28-OCT-1998; 98US-0106072.
 PR 28-OCT-1998; 98US-0106073.
 PR 28-OCT-1998; 98US-0106074.
 PR 28-OCT-1998; 98US-0106087.
 PR 02-NOV-1998; 98US-0106587.
 PR 02-NOV-1998; 98US-0106588.
 PR 02-NOV-1998; 98US-0107034.
 PR 02-NOV-1998; 98US-0107035.
 XX (CONN-) CONNAUGHT LAB LTD.
 XX Mordin AD, Oomen RP, Wang J;
 PI WPI, 2000-350688/30.
 DR P-PSDB; AAY92818.
 XX Chlamydia antigens and the proteins they encode, useful for
 PT vaccinating against Chlamydia infections that affect the respiratory
 tract
 Claim 2; Fig 1; 226pp; English.
 XX The nucleic acids may be used for the recombinant production of the
 CC Chlamydia polypeptides (either in vivo or in vitro) according to standard
 CC recombinant DNA methodologies. The polypeptides may then be used to
 CC vaccinate against Chlamydia infections in mammals. Chlamydia, such as
 CC C. pneumoniae, are pathogens responsible for upper respiratory tract
 CC infections such as community acquired pneumonia, acute respiratory
 CC disease and bronchitis and may be implicated in atherosclerotic changes
 CC and asthma. The nucleic acids may also be used as probes for detecting
 CC the presence of Chlamydia nucleic acids in samples (and therefore
 CC diagnose infections) and the proteins may be used as antigens for the
 CC production of antibodies that may be used to detect Chlamydia proteins
 CC in samples (e.g. via enzyme linked immunosorbent assay (ELISA)).
 XX
 XX Sequence 2526 BP; 693 A; 493 C; 601 G; 739 T; 0 other;
 Alignment Scores:
 Pred. No.: 3,126-315 Length: 2526
 Score: 4295.00 Matches: 841
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0
 US-09-830-446-27 (1-841) x AAA28691 (1-2526)

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 DB 481 AAGTATTAATTCAGACAAATTTCTCAACAGAGAGGCGGAGCAATTAATTCAGAGGC 540
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 DB 781 AACGGAACCGTCTCTCATATGCTATGTTAAGAACTAAGGCTAAGTAACCTGCTTA 840
 QY 281 ArgAlaAlaGlnGlyHisThr11LeuThrPheThrAspPro11LeThrValThrGlySerThr 300
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 RESULT 2
 ABL91253
 ID ABL91253 standard; DNA; 2526 BP.
 AC ABL91253;
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 DT 29-JUL-2002 (first entry)
 XX
 DE Chlamydia pneumoniae cp6270 ORF DNA, SEQ ID NO:140.
 XX
 KW Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
 KW human respiratory disease; cardiovascular disease; atherosclerosis;
 KW coronary artery disease; carotid artery stenosis; myocardial infarction;
 KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
 KW strain CWL029; open reading frame; ORF; gene; ds.
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 FT 55..2523
 FT /*tag= c
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 PD 10-JAN-2002.
 XX
 XX
 PF 03-JUL-2001; 2001MO-IB01445.
 XX
 PR 03-JUL-2000; 2000GB-0016363.
 PR 11-JUL-2000; 2000GB-0017047.
 PR 21-JUL-2000; 2000GB-0017983.
 PR 07-AUG-2000; 2000GB-0019348.
 PR 16-AUG-2000; 2000GB-0020440.
 PR 14-SEP-2000; 2000GB-0022583.
 PR 10-NOV-2000; 2000GB-0027549.
 PR 22-DEC-2000; 2000GB-0031706.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Rattl G, Grandi G;
 XX
 DR WPI; 2002-154726/20.
 DR N-PSDB; ABB90595.
 XX
 PT Novel Chlamydia pneumoniae protein useful in the manufacture of a
 PT medicament for treatment or prevention of infection due to Chlamydia,
 PT preferably Chlamydia pneumoniae, and for diagnostic purposes -
 XX
 PS Claim 5; Page 110-111, 364pp; English.
 XX
 CC Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
 CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
 CC them. The proteins are predicted to be immunogenic and may therefore be
 CC useful in vaccine production and for diagnostic purposes. Chlamydia
 CC pneumoniae is a common cause of respiratory disease in humans, and is
 CC also involved in the development of cardiovascular diseases such as
 CC atherosclerosis, coronary artery disease, carotid artery stenosis,
 CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
 CC claudication and stroke. The proteins and nucleic acids of the invention

CC may be used in vaccines and pharmaceutical compositions for the
 CC prevention or treatment of chlamydial infections, particularly Chlamydia
 CC pneumoniae infections. The proteins may also be used in the detection of
 CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
 CC DNA probe assay or blotting techniques for determining Chlamydia
 CC pneumoniae gene expression. The present sequence represents a
 CC specifically claimed DNA which encodes a Chlamydia pneumoniae protein of
 CC the invention.

XX Sequence 2526 BP; 693 A; 493 C; 601 G; 739 T; 0 other;

Alignment Scores:

Pred. No.:	3,12e-315	Length:	2526
Score:	4295.00	Matches:	841
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-830-446-27 (1-841) x ABL91253 (1-2526)

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DB 301 TTTAGCAATATCGATCAACCAAGGCTTCGAGGCTGCTATTGGAAGTGAAGCAAGCTAAT 360
QY 121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
DB 361 AAGACAGTCACGTTATCAGGATTTTCGGCACTTTCTTTCTTAAATCCCCACCAAGTTACA 420
QY 141 ValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAsnAsp 160
DB 421 GTGACTAAATGAGATTGGAGCTACTCAATGTTAAAGGAATTTAAAGCTTATGTAATGAT 480
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QY 181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerThrArg 200
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QY 201 GlyGlyAlaIleIleThrLysAsnLeuThrLeuSerSerGlyGlyGlyLysThrLeuPheGln 220
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QY 221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyAlaIleAlaIleAlaAspSerGly 240
DB 661 GGGAAATACAGCGCTACGCGCTGCTGTAAGAGAGGCTATGCGCATTCAGACTCTGGC 720
QY 241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAla 260
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QY 281 ArgAlaAlaGlnGlyHisThrIleTyPheTyAspProIleThrValThrGlySerThr 300
DB 841 CGTCTGGCGAAGGACATACATATACCTTTATATATGATTCGATTAACGATACGAGACACA 900
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 RESULT 3 AAA28690 ID AAA28690 standard; DNA; 2750 BP. XX XX AAA28690; XX AC XX DT 29-AUG-2000 (first entry) XX DE C. pneumoniae CPN100397 gene. XX KW Antigen; anti-inflammatory; respiratory; antibacterial; anti-aesthetic; XX KW anti-arteriosclerotic; vaccine; ds. XX OS Chlamydia pneumoniae. XX XX Key Location/Qualifiers XX FT CDS 101..2626 XX FT /*tag= a XX XX WO200024765-A2. XX PD 04-MAY-2000. XX PF 28-OCT-1999; 99MO-CA00992. XX RF 28-OCT-1998; 98US-0106034. XX RR					

PR	28-OCT-1998:	98US-0106039.
PR	28-OCT-1998:	98US-0106042.
PR	28-OCT-1998:	98US-0106044.
PR	28-OCT-1998:	98US-0106072.
PR	29-OCT-1998:	98US-0106073.
PR	29-OCT-1998:	98US-0106074.
PR	29-OCT-1998:	98US-0106087.
PR	29-OCT-1998:	98US-0106087.
PR	02-NOV-1998:	98US-0106587.
PR	02-NOV-1998:	98US-0106588.
PR	02-NOV-1998:	98US-0107034.
PR	02-NOV-1998:	98US-0107035.
PA	(CONN-) CONNAUGHT LAB LTD.	
PI	Muridin AD, Oomen RP, Wang J;	
XX	WPI; 2000-350688/30.	
DR	P-PSDB; AAY92818.	
XX		
PT	Chlamydia antisera and the proteins they encode, useful for	
PT	vaccinating against Chlamydia infections that affect the respiratory	
PT	tract	
XX		
PS	Claim 2; Fig 1; 226pp; English.	
XX		
CC	The nucleic acids may be used for the recombinant production of the	
CC	Chlamydia polypeptides (either in vivo or in vitro) according to standard	
CC	recombinant DNA methodologies. The polypeptides may then be used to	
CC	vaccinate against Chlamydia infections in mammals. Chlamydia, such as	
CC	C. pneumoniae, are pathogens responsible for upper respiratory tract	
CC	infections such as community acquired pneumonia, acute respiratory	
CC	disease and bronchitis and may be implicated in atherosclerotic changes	
CC	and asthma. The nucleic acids may also be used as probes for detecting	
CC	the presence of Chlamydia nucleic acids in samples (and therefore	
CC	diagnose infections) and the proteins may be used as antigens for the	
CC	production of antibodies that may be used to detect Chlamydia proteins	
CC	in samples (e.g. via enzyme linked immunosorbant assay (ELISA)).	
XX		
SQ	Sequence 2750 BP; 756 A; 532 C; 641 G; 821 T; 0 other;	
Alignment Scores:		
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Percent Similarity:	100.00%	Conservative: 0
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US-09-830-446-27 (1-841) x AAA28690 (1-2750)		
QY	1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20	
Db	101 ATGAAATTCACCTCCGCTTTTATTTATGATATCATTAGACTACGCTTTCTATGTGAAT 160	
QY	21 LeuLeuGlyAlaIleThrThrGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40	
Db	161 TTATTGGAGCGCTACTACCGAAGAGTTATTCGGCTGCAATAGCTTCGATGGAACTACA 220	
QY	41 SerThrThrSerPheSerSerIleThrSerSerAlaThrAspGlyThrAsnArgValPhe 60	
Db	221 TCACCAACACAGCTTTCTTGTAAACATCATCGGCTACAGTGGACACCAATTATGTTTTT 280	
QY	61 LysAspSerValIleIleGluAsnValProIleThrGlyIleThrGlnSerThrSerCys 80	
Db	281 AAAGATCTTGATGTTATGAAATGTACCCAAAACAGGGGAAATCAGTCTACTAGTTGT 340	
QY	81 PheLysAsnAspAlaIleAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThr 100	
Db	341 TTTAAAAATGAGCGCTGACGCTGAGATCTAAATTTCTTAGAGGGGGATTTTCTTTCACA 400	
QY	101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaIleIleGlySerGlyAlaIleAsn 120	
Db	401 TTTAGCAATATGATGACCAACCGCTTCTGAGCTGCTATTTGAACTGAAGCAAGCTAAT 460	

121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
 461 AAGACGTCACGTTATCAAGATTTTCGACATTTCTTTCTTAATATCCCAAGCACTACA 520
 141 ValThrAsnGlyLeuGlyValAlaLeuValLysGlyAsnLeuSerLeuLeuAspAsp 160
 521 GTGACATAATGATGGAGCTATCAATGTTAAAGGAAATTTAAGCTATTTGATATGAT 580
 161 LysValLeuLeuGluAspAsnPheSerThrGlyAspGlyGlyValAlaLeuGlyValAlaGly 180
 581 AAGGATTAATTCAGACCAATTTCTCAACAGAGAGAGCGGAGCAATTAATGTGACGCG 640
 181 SerLeuLysLeuAlaAsnAsnLysSerLeuSerPheLeuGlyAsnSerSerThrArg 200
 641 TCTTGAAAGATGGCAAAACATAAGTCCCTTTCTTAATGAAATAGTTCTTCAACACGT 700
 201 GlyGlyValAlaLeuIleThrLysAsnLeuThrLeuSerSerGlyGlyLeuThrLeuPheGln 220
 701 GCGCGAGCATTCATACCAAAAACCTCACACTATCTTGCGGGAACCTCATTTGAG 760
 221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyValAlaLeuAlaLeuAspSerGly 240
 761 GGAATACAGCGCTACGCGCTGCTGTAAGAGAGGTCTATCGCATTCGACACTCTGCG 820
 241 ThrLeuSerIleSerGlyAspSerGlyAspIleAlaPheGlyGlyValThrIleGlyAla 260
 821 ACCCTATCATTTCTGAGACACAGTGGCACTTATCTTTAGAGCAATACGATAGAGCT 880
 261 ThrGlyThrValSerIleSerAlaLeuAspLeuGlyThrSerAlaLysIleThrAlaLeu 280
 881 AAGAGAACCGTCTCTCATAGTGTCTATGATTAGAACTAGCGCTAAGATTAAGTGGTTA 940
 281 ArgAlaAlaGlyGlyIleThrIleThrPheThrAspProIleThrValThrGlySerThr 300
 941 CGGCTGCGCAAGACATACGATATACCTTTATGATCCGATACGTAACAGATTCGACA 1000
 301 SerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGlyThr 320
 1001 TCTGTTGCTGATGCTCTCAATATTAATACCTCGATACGAGATTAACAAGATTAAG 1060
 321 GlyThrIleValPheSerGlyGlyLysLeuThrGlyAlaGlyAlaLysAspGlyLysAsn 340
 1061 GGAACCATAGTCTTTCTGGAGAGAGCTCACGAGGCGAAGCTAAAGATGAAGAAGAC 1120
 341 ArgThrSerLysLeuGlnAsnValAlaPheLysAsnGlyThrValValLeuLysGly 360
 1121 CGCACTTCTAAATTAATCTCAAAATGTTGCTTTAAATGGAAGCTGATTTTAAAGGT 1180
 361 AspValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAsp 380
 1181 GATGCTGTTTAAGTCGAAACGCTTCTCTCAAGATGCAAACTTAAGTTGATTAAGAT 1240
 381 LeuGlyThrSerLeuValAlaAsnThrGlySerIleGlyLeuThrAsnLeuGlyLysAsn 400
 1241 TTAGGGAACGTCGTGGTCAAAACACCAAGATGAGTTAAGCAATTTGGAATTAAT 1300
 401 IleAspSerLeuAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlyLysAsp 420
 1301 ATAGACTCTCTCAAGAACGGAAGAAAGATTAACCTAGTGTGCCACACTCGAAGAAAGT 1360
 421 IleArgIleAspArgProValValLeuAlaIleSerAspGlySerPheThrGlnAsnGly 440
 1361 ATTCGATAGATGCTGCTGTTGACTGCAATTAAGGATGAGAGTTTATTCAAATGCG 1420
 441 PheLeuAsnGlyAspIleSerThrAspGlyIleLeuGlyLysAspAlaGlyLysAspIle 460
 1421 TTTTGAATGAGAGCAATTCCTATGATGGGATCTTGAGTTAGATCTCGGAAAGACATC 1480
 461 ValIleSerAlaAspSerArgSerIleAspAlaValGlnSerProGlyThrGlyGly 480
 1481 GTGATTTCTGACGATTCGACGATATGATGCTGTAACAATCTCCGATGCTATACGAGA 1540

481 LysTrpThrIleAsnTrpSerThrAspAspLysLysAlaThrValSerTrpAlaLysGln 500
 1541 AAGTCAGACATCAATTTGCTATGATGATTAAGAAAGCTACGTTCTTGCGCAAGCAG 1600
 501 SerPheAsnProThrAlaGlyGlnGlyAlaProLeuValProAsnLeuLeuTrpGlySer 520
 1601 AGTTTAAATCCCACTGCGAGAGAGAGGCTCCGTTAGTCTCAATCTCTTGGGGTCT 1660
 521 PheIleAspValArgSerPheGlnAsnPheIleGlyLeuGlyThrGlyGlyValaProThr 540
 1661 TTTATGATGTTGCTTCTTCCAGATTTTATAGACTAGGATCTGAAGCTCTCTTAC 1720
 541 GlyLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArgGlnAsn 560
 1721 GAAAGAGATTTTGCTTGACGAGCATTTCCAATGTTTGCATAGAGACGCTGTGAAT 1780
 561 GlnArgLysPheAsnGlyValSerGlyGlyValAlaValAlaGlyAlaSerThrArgMetPro 580
 1781 CAAGGAAATCCGTCATGATGAGAGAGTGTGATGATGATGATGATGATGATGATGATGAT 1840
 581 GlyLysAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspThrPhe 600
 1841 GGTGATGATACCTTGTCTGAGTTTGTCTCAAGCTTTTGCGCGGACAAAGACTACTTT 1900
 601 MetAsnThrAsnPheAlaLysThrThrAlaGlySerLeuArgLeuGlnHisAspAlaSer 620
 1901 ATGATATCAATTTGCAAGACCTACCGAGATCTTACGTTTGCACAGATCTCTCC 1960
 621 LeuTrpSerValValSerIleLeuLeuGlyGlyGlyLysLeuArgGlyLysLeuLeuPro 640
 1961 CTATCTCTGTGAGATACCTTTTATAGAGAGGAGACCTCCGGAATCTGTGCT 2020
 641 TyrValSerLysThrLeuProCysSerPheThrGlyGlyLysLeuSerThrGlyIleThrAsp 660
 2021 TATGTTCCAAAGCTCTGCTGCTCTTTCTATAGAGAGCTTACGCTTACGCTATCGAT 2080
 661 HisArgMetLysThrGlySerLeuProProProProThrLeuSerThrAspIleThr 680
 2081 CATGCAAGAGACCGAGCTCTACCCCCCCCCCGAGCGCTCTCCAGCATCATACT 2140
 681 SerTrpGlyGlyThrValTrpAlaGlyGlyLeuGlyThrArgValAlaValGlnAsnThr 700
 2141 TCTTGGGAGATATGCTGCGGCTGAGAGCTGGAGACTCGATGCTGTTGAAATATCC 2200
 701 SerGlyArgGlyPhePheGlnGlyThrProPheValLysValGlnAlaValTyrAla 720
 2201 ACGGCAAGAGATTTTCCAAAGATCACTCCATTTGTAAGTCCAAAGCTGTTTACGCT 2260
 721 ArgGlnAspSerPheValGlyLeuGlyValAlaIleSerArgAspPheSerAspSerHisLeu 740
 2261 CGCCAAAGATAGCTTTGTGAAGCTAGAGCTATCACTCGATTTTATGATTCGATCTT 2320
 741 TyrAsnLeuAlaIleProLeuGlyIleLysLeuGlyLysArgPheAlaGlyGlnIleTyr 760
 2321 TATAACTCTGCAATCTCTTGGAAATCAAGTTAGAAACGCTTTGCGAGCAAAATTAAT 2380
 761 HisValValAlaMetThrSerProAspValCysArgSerAsnProLysCysThrThrThr 780
 2381 CATGTTGATGATATTTCTCCAGATGTTGCTAGATGTTGCTAGATGTTGCTAGATGTTGCT 2440
 781 LeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsnLeuAlaArgGlnAlaGly 800
 2441 CTACTTTCACCAAGGAGGATTTGAAAGCAAAAGTTTGAACCTTGAAGACAGGCTGCT 2500
 801 IleValGlnAlaSerGlyPheArgSerLeuGlyValAlaAlaGlyLeuPheGlyLysPhe 820
 2501 ATGTTTCAAGGCTCAGGTTTTCGATCTTTGGAGCTGAGCAGACCTTTCCGGAACTTT 2560
 821 GlyPheGlyTrpArgGlySerSerArgSerThrAsnValAspAlaGlySerLysIleLys 840
 2561 GCTTGAATGCGGGAGATTTCTGATGCTATGATGATGATGATGATGATGATGATGATGAT 2620
 841 Phe 841

Db 2621 TTT 2623

RESULT 4
AA06819
ID AAX06819 standard; DNA; 2526 BP.
XX

AC AAX06819;
XX
DT 26-APR-1999 (first entry)
XX

Chlamydia pneumoniae surface exposed protein Omp7 DNA.
XX
KW Omp7; outer membrane protein 7; surface exposed protein; antigen;
infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
OS Chlamydia pneumoniae.
XX
PN W09658953-A2.
XX
PD 30-DEC-1998.
XX
PF 19-JUN-1998; 98MO-DK00266.
XX
PR 23-JUN-1997; 97DK-0000744.
XX

(BIRK/) BIRKELUND S.
PA (CHRI/) CHRISTIANSEN G.
XX
PI Birkelund S, Christiansen G, Knudsen K, Madsen A,
PI Mylund P;
XX
DR WPI; 1999-105610/09.
DR P-PSDB; AAW88420.
XX

Species-specific test for identifying mammals infected with
PT Chlamydia pneumoniae - comprises detecting antibodies specific for
PT outer membrane proteins of C. pneumoniae or nucleic acids encoding
PT these proteins

Claim 6; Page 49-50; 115pp; English.

This DNA sequence codes for the novel 89.7 kDa surface exposed
CC protein Omp7 (see AAW88420) of the human respiratory pathogen
CC Chlamydia pneumoniae. By generating antibodies against C.
CC pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
CC was obtained which reacted with outer membrane proteins. The
CC antibody was used to identify the genes (see AAX06816-27) encoding
CC Omp4-Omp15 proteins (see AAW88417-28) in an expression library of
CC C. pneumoniae DNA. The genes are situated in 2 gene clusters:
CC Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
CC the other, and encode polypeptides of about 89.6-100.3 kDa and
CC about 56.1 kDa. The invention provides a new species specific test
CC for identifying mammals (including humans) infected with Chlamydia
CC pneumoniae. The test comprises detecting antibodies specific for
CC Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
CC membrane proteins, especially by PCR. The proteins are also used
CC in the diagnosis of C. pneumoniae infection in mammals. The
CC nucleic acids and proteins can also be used in the immunisation of
CC mammals, the nucleic acids being particularly useful as DNA
CC vaccines for effecting in vivo expression of antigens. The
CC vaccines may also prevent atherosclerosis and bronchial asthma,
CC which are possibly associated with C. pneumoniae.
XX

Sequence 2526 BP; 696 A; 495 C; 597 G; 738 T; 0 other;
XX

Alignment Scores:
Pred. No.: 6, 04e-314 Length: 2526
Score: 4278.00 Matches: 837
Percent Similarity: 99.888 Conservative: 3
Best Local Similarity: 99.528 Mismatches: 1
Query Match: 99.608 Indels: 0
Gaps: 0

US-09-830-446-27 (1-841) x AAX06819 (1-2526)

QY 1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAen 20
Db 1 ATGAAGATTCCACCTCCGCTTTTATTGATATCATTAAGTACCACTTCTTATGTCGAAT 60

QY 21 LeuLeuGlyValAlaIleThrThrGluLeuSerAlaSerAenSerPheAspGlyThrThr 40
Db 61 TTATTAGAGAGCTGCTACTACCGAAGAGCTATCGCTACCAATAGCTGATGGAAGTACA 120

QY 41 SerThrThrSerPheSerSerIleThrSerSerAlaThrAspGlyThrAsnYrAlaPhe 60
Db 121 TCACACACAGAGCTTTTCTAGTAAACATCCGCTACAGATGACCAATATATTTT 180

QY 61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCys 80
Db 181 AAGATTCTGTAGTATTAGAAAATGTACCAAAACAGGGGAACTCAGTCTAGTTGT 240

QY 81 PheLysAsnAspAlaAlaIleGlyAspLeuAsnPheLeuGlyGlyPheSerPheThr 100
Db 241 TTTAAATAATGACGCTGACGCTGAGATCTAATTTCTTAGAGGGGGAATTTCTTACA 300

QY 101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAsn 120
Db 301 TTTAGCAATATGATGACCAACGCGCTTCTGAGCTGCTATTGGAAGTGAACACCTAAT 360

QY 121 LysThrValIleThrSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
Db 361 AAGACAGTCACGTTATACGAGATTTTGGACCTTCTTTTAAATCCCAACCAAGTACA 420

QY 141 ValThrAsnGlyLeuGlyValAlaIleAsnValLysGlyAsnLeuSerLeuAspAsnAsp 160
Db 421 GTGACTAATGATGCTGGAGCTATCAATGTTAAAGGAATTTAAGCTATGATATGAT 480

QY 161 LysValIleuIleGlnAspAsnPheSerThrGlyAspGlyGlyValIleAsnCysAlaGly 180
Db 481 AAGGATTGATTCAGAGCAATTTCTCAACAGAGATGCGGAGCAATTAATTTGTCCAGGC 540

QY 181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerThrArg 200
Db 541 TCTTGAAAGATCGCAACAAATTAAGTCCCTTCTTTATTTAGAAATAGTTCTTCAACACT 600

QY 201 GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220
Db 601 GCGGAGGATTCATACCAAAACTCAGCATGTTCTGCGGGGAACTATTTACG 660

QY 221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAspSerGly 240
Db 661 GGGATTAACAGCGCTACGCGCTGCTGTAAAGAGGTGCTATCGCATTCAGACTCTGCGC 720

QY 241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAla 260
Db 721 ACCCTATTCATTTCTGAGACAGTGGCGACATTACTTTGAAGGCAATACGATAGAGCT 780

QY 261 ThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeu 280
Db 781 ACAGAAACCGTCTCTCAATAGTCTATTTGATTTAGGAACCTAAGCGCTAAGTACGCTTA 840

QY 281 ArgAlaAlaGlnGlyHisThrIleThrPheThrAspProIleThrValThrGlySerThr 300
Db 841 CGTGCTGGCAAGACATACATATATCTTTATGATTCGATATCTGTAACAGATGACACA 900

QY 301 SerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGluThrThr 320
Db 901 TCTGTGCTGATGCTCTCAATATTAATAGCCCTGATACGAGATACAAAGATTAACG 960

QY 321 GlyThrIleValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGlyLysAsn 340
Db 961 GGAACCATATGCTTTTCTGAGAGAACTCAGCGAGGCAAGAGCTTAAGATGAAGAAGAC 1020

QY 341 ArgThrSerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeuLysGly 360

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Db      1021 CGCACTCTCAAAATTAATCTCAAAATGTTGTTTAAAAAATGGGAGCTAGTTTAAAGAT 1080
Qy      361  ASPPVALLIUSERRALAAANGIYPHESERGINAARPAIAASERLYLEULILEMETAP 380
Db      1081 GATGTCGTTTAAAGCGAAACGGTTTCTCTCAGAGATGCAACCTTAAGTATGATATGAT 1140
Qy      381  LEUGLYTHSERLEUVALAIAANTHRSUGSERILEGLUEUTHASMLEUGIULIEN 400
Db      1141 TTAGGAGACCTGCTTGTTGTTGCAACACCGAAAGTATCGAGTTACCAATTTGAAATTAAT 1200
Qy      401  ILEAPSERLEUARGANGIYLYLYLYLYLYLYLYLYLYLYLYLYLYLYLYLYLYLYLY 420
Db      1201 ATAGACTCTCTCAGAGACCGGAAAGATTAATACTCAGTGTGCGACAGCTCAGAAAGAT 1260
Qy      421  ILEAGGILEAPARGPROVALIALLIUSERRASERPHETRYGILNANGIY 440
Db      1261 ATTCGTATAGATGCTGCTGTTGTTACTGCGAATTAAGATGAGATGAGATTTTATCAAAATGCG 1320
Qy      441  PHELEUANGIUSAPHISERTYRAPHGIYILEUGIULIUSAPALAGIYLYSAPILIE 460
Db      1321 TTTTGAATGAGACCATTCCTATGATGGGATTTCTTGAGTTAGATGCTGCGAAAGCATC 1380
Qy      461  VALIIESERIALAASERARGSERILEAPALAVAGINSEPROTYGILYTYGINGIY 480
Db      1381 GTGATTTCTGCAGATTTCTGCAGATTAATATGCTGTACATCTCCGTATGCTATCAGGGA 1440
Qy      481  LYSTPTTHRIEANTTPSERTHRSAPAPLYLYLYLYLYLYLYLYLYLYLYLYLYLYLY 500
Db      1441 AAGTGACACATCAATGATGCTACTAGATGATGATGATGATGATGATGATGATGATGAT 1500
Qy      501  SERPHEAENPROTHRALAGIUGINGIUALAPROLEUVALPROASMLEUENUTRPGIYSE 520
Db      1501 AGTTTAAATCCCACTGCTGAGAGAGAGGCTCCGTTAGTTCTTAATCTTTTGGGGTTCT 1560
Qy      521  PHEIIEAPVALARGSERPHEGINAPHEIIEGLUEUGIYTHRGILUGIYALAPROYR 540
Db      1561 TTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
Qy      541  GIULYARGPHEPTRVALIAGIYIIESERAPVALIENHIAARGSERIYTRGILUGAN 560
Db      1621 GAAAGAGATTTTGGTTGCTGAGGCAATTCGAATGTTTGCATAGAGACCGGTGTAAGAT 1680
Qy      561  GINARGLYPHEARGHIAVALSERGIYIYALAVAIAGIYALASERTHARGHECTPRO 580
Db      1681 CAAGGAAATTCCTGCTATGATGAGGAGGCTGCTGATGATGATGATGATGATGATGATG 1740
Qy      581  GIYGIYASPTTHRLEUSERLEUGIYPHEALAGIULEUPHEALARGAPLYSAPTYRPH 600
Db      1741 GGTGGGATACCTTGTCTGGGTTTGTCTCAGCTCTTGGCGGTGACAAAGACTACTT 1800
Qy      601  METASNTTHASNPHEALAYETHRYTRALAGIYSELEUARGLEUGINIHASAPLASER 620
Db      1801 ATGAATTAACCAATTTCCGAAAGACTTAAGCAGATCTTACGTTTGACAGACATGCTTCC 1860
Qy      621  LEUTYRSEVALIASERIIELEUGIYGIUGIYIYLEUARGIULIIELEUENUTR 640
Db      1861 CTRTACTCTGTGTGATGATCTCTTTTAAAGAGAGGAGACTCCGCGAATCTCTGTGGCT 1920
Qy      641  TYRVALSERLYSETHRLEUPROCYSESPHETRYGIYGIULEUSERTYGIYHISHTHAP 660
Db      1921 TATGTTTCAAGACTCTGCGCGTGTCTTTCTATAGGCACTTATGATGATGATGATGAT 1980
Qy      661  HISARGMETLYSETHRGIUSERTLEUPROPROPROPROPROTHRLEUSERTHRSAPHIS 680
Db      1981 CATCGATTAAGACCAAGCTCTACACCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 2040
Qy      681  SETTRGILYGIYTYRVALIYTRPALAGIYGIULEUGIYTHARGVALIYALAGIUAENTH 700
Db      2041 TCTTGGGAGAGATATGCTGCTGAGGAGCTGAGGAGCTGAGGAGCTGCTGTTGAAATACC 2100
Qy      701  SERGIYARGGIYPHEPHEGINGIYTYRTHRPHOVALIYVALIYVALIYVALIYVALIY 720
Db      2101 AGCGGAGAGAGATTTTCCAGAGATACACTCACTTTGTAAGTCCAAAGCTGTTTACTCG 2160

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Qy      721  ARGILNAPSERPHEVALGIULEUGIYALIIESERARGAPPHESERASPSEHISLEU 740
Db      2161 CGCCAAATAGCTTTGTTGAACCTAGAGCTATGCTGATATTTAGATATTCGATCTT 2220
Qy      741  TYRANLEUALAIIEROLEUGIYIIEYSELEUGIULYARGPHEALAGIUGINTYTRY 760
Db      2221 TATAACTTGGCATTCCTCTTGAATCAAGTTAGAGAAACGGTTTGACAGAGCAATATAT 2280
Qy      761  HISVALIYALAMETLYRSETPROAPVALCYARGSERANPOLYCYETHRTHRTHR 780
Db      2281 CATGTTGAGGAGATATCTCCAGATGTTGTGTGATGAACCCCAATGTACAGACTACC 2340
Qy      781  LEUUSERRANGINGIYSETRIPLYETHRYSGLYSEANLEUALAARGIYALAGIY 800
Db      2341 CTACTTCCAAACCAAGGAGTGGAGAACCAAGCTTGACACTTACAGAGACAGGCTGCT 2400
Qy      801  ILEVALGINALASERGIYPHEARGSERLEUGIYALIAALAGIULEUPHEGIYASNPHE 820
Db      2401 ATGTTTCAAGGCTCAGGTTTTCATCTTTGGGAGCTGCAGACAGACTTTTCGGGAACTTT 2460
Qy      821  GLYPHEGIUTRPAIGIYSETRARGSERTRYRANVALIAPALAGIYSETRILELYS 840
Db      2461 GGCCTTGAATGCGCGGATCTTCTGATGATATGATGATGATGATGATGATGATGATG 2520
Qy      841  PHE 841
Db      2521 TTT 2523

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RESULT 5

AA91990 ID AAX91990 standard; DNA; 1230025 BP.

AA91990; 13-SEP-1999 (first entry)

DT 13-SEP-1999 (first entry)

DE Nucleotide sequence of the complete genome of Chlamydia pneumoniae.

KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;

KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis;

KW vaccine; neutralising epitope; ss.

OS Chlamydia pneumoniae.

PN MO9927105-A2.

PD 03-JUN-1999.

PF 20-NOV-1998; 98MO-IB01890.

PR 04-NOV-1998; 98US-0107078.

PR 21-NOV-1997; 97FR-0014673.

PA (GENEST) GENEST.

PI Griffaia R.

DR WPI; 1999-357842/30.

PT Genome sequence of Chlamydia pneumoniae

PS Claim 1; Page 291-611; 1912pp; English.

CC The present sequence represents the complete genome of Chlamydia pneumoniae, and encodes proteins AA934584-Y35879. C. pneumoniae causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the C. pneumoniae genome (see CC AA934584-Y35879) can be used in immunogenic compositions as vaccines. CC Vectors containing C. pneumoniae nucleotide sequences can also be used as immunogenic compositions, especially where the vector directs

CC the expression of a neutralizing epitope of C. pneumoniae.

XX Sequence 1230025 BP; 367213 A; 249833 C; 249013 G; 363589 T; 377 other;

Alignment Scores:

Pred. No.:	8e-309	Length:	1230025
Score:	4255.00	Matches:	840
Percent Similarity:	99.76%	Conservative:	0
Best Local Similarity:	99.76%	Mismatches:	1
Query Match:	99.07%	Indels:	2
DB:	20	Gaps:	0

US-09-830-446-27 (1-841) X MAX91990 (1-1230025)

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QY      1 MetLysIIProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
DB      28950 ATGAAAGATTCCTCCGCTTTTATGATACATGATGACTTACGCTTCTATGTCGAAT 29009
QY      21 LeuLeuGlyAlaIleThrThrGluGluLeuSerIleSerAsnSerPheAspGlyThrThr 40
DB      29010 TTATTAGGAGCTGCTCTACCAAGAGTTATCGGCTTAGCAATAGCTTCGATGCACTACA 29069
QY      41 SerThrThrSerPheSerSerIleThrSerSerAlaThrAspGlyThrAsnIleValPhe 60
DB      29070 TCACACACACAGCTTTCTAGTAAACATCATCCGCTACAGATGCGACCAATTATGTTTTT 29129
QY      61 LysAspSerValValIleGluAsnValProLeuThrGlyGluThrGlnSerThrSerCys 80
DB      29130 AAGAGATTCGTAGTATGAAAAATGTAACCAAAACAGGGGAAACTCAGTCTACTAGTTGT 29189
QY      81 PheLysAsnAspAlaAlaIleGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThr 100
DB      29190 TTTAAATATACCTCTGAGCTGAGATCTAAATTTCTTAGAGAGGGGATTTCTTTCACA 29249
QY      101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAsn 120
DB      29250 TTTAGCAATTCATGATGCAACACAGGCTTCGAGCTCTATTGGAAGTGAAGAGCTAAT 29309
QY      121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuIleSerProAlaSerThr 140
DB      29310 AAGACAGTCAAGTTATCAGGATTTTCGGCACTTTCTTAAATCCCAAGCAAGTACA 29369
QY      141 ValThrAsnGlyLeuGlyAlaIleAsnValIleGlyAsnLeuSerLeuAspAsp 160
DB      29370 GTGACTATATGATTGGAGCTATCAATGTTAAAGGAATTTAAACCTATGCTATGAT 29429
QY      161 LysValLeuIleGlnAspAsnPheSerThrGlyAspGlyAlaIleAsnGlyValGly 180
DB      29430 AAGGATTCATTCAGGACATTTCTCAACAGAGATGCGGAGCA-ATTATTCGCGAGGC 29488
QY      181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerThrArg 200
DB      29489 TCCCTGAAGATCCCAACAAATAGTCCCTTTTATGAAATAGTTCTTCAACACGT 29548
QY      201 GlyGlyAlaIleIleThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220
DB      29549 GCGGAGCACTTCAATACCAAAACCTCACTATCTTCTGTGGGAAACCTCATATTTCCAG 29608
QY      221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyAlaIleAlaIleAlaAspSerGly 240
DB      29609 GGGAAATACAGCGCTACGCGCTCGTGAAGAGAGTCTATCCGATGCAAGCTCGGC 29668
QY      241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAla 260
DB      29669 ACCCTATCCATTTCTGAGACAGTGGGACATTAATCTTTAAGGACATACGATAGAGGCT 29728
QY      261 ThrGlyThrValSerIleSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeu 280
DB      29729 ACAGGAACCGTCTCTCATATGCTATTGTAAGAACTAGCCGATGATACGCTGCTTA 29788
QY      281 ArgAlaAlaGlnGlyIleIleThrIleIlePheIleAspProIleThrValThrGlySerThr 300
DB      29789 CGTGTGCGGAGGACATACGATATACTTTATGATCGATTCTGTAAACAGGATGAGCA 29848

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QY      301 SerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGlyThr 320
DB      29849 TCTGTGCTGATGCTCTCAATATTAATAGCCCGATACAGATATAACAAAGATACG 29908
QY      321 GlyThrIleValPheSerGlyGlyLysLeuThrGluAlaGluAlaLysAspGlyLysAsn 340
DB      29909 GGAACCATAGTCTTTCTCGAGAGGAGCTCAACGAGGACAGAACTAAAGATGAGAAAGAC 29968
QY      341 ArgThrSerIleLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeuLysGly 360
DB      29969 CGCATTCTAAATTAATCTCAAAATGTGCTTTTAAATAAGGACGTAGTTGAAAGG 30028
QY      360 LysValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAs 380
DB      30029 TGAATCGTTTAAAGCCAGACGCTTCTCTCAGATGCAAACTTAAGTTGATTATGCA 30088
QY      380 PheGlyThrSerLeuValAlaAsnThrGlnSerIleGluLeuThrAsnLeuGluIleAs 400
DB      30089 TTTAGGAGCGTGGTGTGTCGAAACACCGAAAGTATCGATTACGAATTTGAAATTAA 30148
QY      400 LysAspSerLeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAs 420
DB      30149 TATGACTCTCTCAGAACGCGGAAAAAGATAAACTCAGTGTCCACAGCTCAGAAAGA 30208
QY      420 PheArgIleAspArgProValValLeuAlaIleSerAspGlySerPheTyrosineGly 440
DB      30209 TATTGCTATAGATCGTCTGCTGTGTACTGCGCAATTACGATGAGAGTTTATCAAAATG 30268
QY      440 LysLeuAsnGluAspIleSerIleAspGlyIleLeuGluLeuAspAlaGlyLysAsp 460
DB      30269 CTTTGTGAATGAGGACATTCCTATGATGGGATTTCTGATTGATGCTGGAAAGCAT 30328
QY      460 ValIleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyrosineGly 480
DB      30329 CGTGAATTCGCGAGATTCCTCGCATGATGCTGTAACAATCCGATAGCTATACAGG 30388
QY      480 LysTrpThrIleAsnTrpSerThrAspAspLysValAlaThrValSerTrpAlaLysGly 500
DB      30389 AAGTGAACGATAAATTTGGTCTATGATGATTAAGAAAGCTACGCTTTCTTGGCGAAGCA 30448
QY      500 nSerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySer 520
DB      30449 GAGTTTAAATCCACAGCTGAGGAGAGGCTCCGTTAGTTCCAACTCTTTGGGGTTC 30508
QY      520 PheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluAlaProTy 540
DB      30509 TTTTATAGATGTTCTGCTTCCAGAAATTTATAGAGCTAGTACGAGAGTCTCTCTTA 30568
QY      540 GlnLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyValArgLys 560
DB      30569 CGAAAGAGATTTTGGGTTGCAAGGCAATTCCAATGTTTGATAGAGAGCGGTCGTGAAA 30628
QY      560 GlnArgLysPheArgHisValSerGlyAlaValAlaValAlaSerThrArgMetPro 580
DB      30629 TCAAGGAATTCGTCATGTAGTGAAGTGTGTAGTAGAGTCAAGACGAGATGCC 30688
QY      580 GlnGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyros 600
DB      30689 GGGTGTGATACCTTCTCTCTGCTGCTTGTGCTAGCTCTTGTCCGCGGACCAAACTACTT 30748
QY      600 eMetAsnThrAsnPheAlaLysThrTyraIleGlySerLeuArgLeuGlnHisAspAlaSer 620
DB      30749 TATGAATACCAATTTGCAAAAGCTACGAGGATCTTACGTTTGACGACCACTGCTTC 30808
QY      620 rLeuTySerValValSerIleLeuLeuGlyGluGlyGlyLysArgGlyLysLeuLeuPhe 640
DB      30809 CCTATACTGTGTGTAGTATCTTTTAGAGAGGAGGAGACTCGGAGATTCCTGTTGCC 30868
QY      640 rTyValSerLysThrLeuProCysSerPheTyrosineGlyGlnLeuSerTyrosineHis 660
DB      30869 TTAATTTCCAAAGACTCGCGGTCTCTTCTATGCGGAGCTTAGCTACGCGCATACGGA 30928

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QY 660 PHISARMEUlyTHrGluSerLeuProProProProThrLeuSerThrAspHisTh 680
DB 30929 TCATGCGATGAAGACGAGGTCTCTACCCCCCCCCCGAGGCTCTGACGAGCATATAC 30988
QY 660 rSerTrpGlyGlyTyrValTTPAlaGlyGluLeuGlyThraValAlaValGluAsnTh 700
DB 30989 TTCCTGGGAGGAGATATGCTGGGCTGAGAGCTGGGAACTCGAGTTGCTTGAATAATAC 31048
QY 760 rSerGlyArgGlyPhePheGlnGluTyrThrProPheValGlnAlaValTyrAl 720
DB 31049 CAGCGGACAGGAGATTTTCCAAAGATACCTCATTTGTAAGTCCAAAGCTGTTTACGC 31108
QY 720 AArgGlnAspSerPheValGluLeuGlyAlaLeuSerArgAspPheSerAspSerHisle 740
DB 31109 TCGCCAAATAGCTTGTATGAGCTAGAGCTATCATGCTGATTTTAGATTCGCAATCT 31168
QY 740 uTyrAsnLeuAlaIleProLeuGlyTyleLeuLeuGlyValArgPheAlaGluGlnTyrTy 760
DB 31169 TTATTAACCTTCGATTCCTCTTGGAATCAAGTAAACGGTTTGCAGACCAATATTA 31228
QY 760 rHisValValAlaMetTyrSerProAspValCysArgSerAspProLysCysThrThTh 780
DB 31229 TCATGTTAGGAGATGATTTCTCCAGATGTTGTGTAGTAAACCCCAATGTACACATAC 31288
QY 780 rLeuLeuSerAengGlnGlySerTrpLysThrLysGlySerAenLeuAlaArgGlnAlaG1 800
DB 31289 CCTACTTTCCAAACCAAGGAGATTTGGAAGCCAAAGTTTGAATTCAGCAAGCAGGCTGG 31348
QY 800 YlleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsnPh 820
DB 31349 TATGTTACGAGCTCAGGTTTTCGATCTTTGGAGAGCTGCAGACAGCTTTTCGGGAATCT 31408
QY 820 eGlyPheGlyUTTPArgGlySerSerArgSerTyrAsnValAspAlaGlySerLysIlely 840
DB 31409 TCGCTTTGAATGCGCGGAGATCTTCTGTAGCTATATGATGATGCGGATGCAAAATCA 31468
QY 840 aspHe 841
DB 31469 ATTT 31472

```

RESULT 6
AAx06830
ID AAX06830 standard; DNA; 1830 BP.
AC AAX06830;
XX 26-APR-1999 (first entry)
DT Chlamydia pneumoniae surface exposed protein Omp7 DNA.
XX Chlamydia pneumoniae surface exposed protein; antigen;
XX Omp7; outer membrane protein 7; surface exposed protein; antigen;
XX infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
XX Chlamydia pneumoniae.
XX MO9858953-A2.
XX 30-DEC-1998.
XX 19-JUN-1998; 98MO-DK00266.
XX 23-JUN-1997; 97DK-0000744.
XX (BIRK/) BIRKELUND S.
XX (CHRI/) CHRISTIANSEN G.
XX Birkelund S, Christiansen G, Knudsen K, Madsen A;
PI Mygind P;
XX WPI; 1999-105610/09.
XX P-PSDB; AAW88431.
XX Species-specific test for identifying mammals infected with

```

PT Chlamydia pneumoniae - comprises detecting antibodies specific for
PT outer membrane proteins of C. pneumoniae or nucleic acids encoding
PT these proteins
PS Disclosure; Page 83-86; 115pp; English.
XX This DNA sequence encodes the novel surface exposed protein Omp7
XX (see AAW88431) of Chlamydia pneumoniae, a human respiratory pathogen.
CC It is described below as a subsequence of a claimed nucleic acid fragment
CC (see AAX06819) encoding Omp7 (see AAW88420). The invention provides a
CC new species specific test for identifying mammals (including
CC humans) infected with C. pneumoniae. The test comprises detecting
CC antibodies specific for surface exposed proteins Omp4-Omp15 (see
CC AAW88417-28) or detecting nucleic acid fragments encoding them (see
CC AAX06816-27), especially by PCR. The proteins are also used in the
CC diagnosis of C. pneumoniae infection in mammals. The nucleic acids
CC and proteins can also be used in the immunization of mammals, the
CC nucleic acids being particularly useful as DNA vaccines for
CC effecting in vivo expression of antigens. The vaccines may also
CC prevent atherosclerosis and bronchial asthma, which are possibly
CC associated with C. pneumoniae.
SQ Sequence 1830 BP; 485 A; 357 C; 443 G; 545 T; 0 other;

Alignment Scores:
Pred. No.: 1,93e-187 Length: 1830
Score: 2603.00 Matches: 532
Percent Similarity: 74.46% Conservative: 22
Best Local Similarity: 71.51% Mismatches: 50
Query Match: 60.61% Indels: 140
DB: Gaps: 8

US-09-830-446-27 (1-841) x AAX06830 (1-1830)
QY 30 leuSerAlaSerAsnSerPheAspGlyThrThrSerThrThrSerPheSerSerLys--- 48
DB 10 TTAGCGAGTCCGACAGTATATATATGATATCAACACACAGAAATTTACTCTTAAGCG 69
QY 49 ThrSerSerAlaThrAspGlyThrAsnTyrValPheLysAspSerValValIleGluAsn 68
DB 70 GCACCTTCTGATGCTAGTGCGACGACCTATATTTCCAGATGGGAGATCTCGATTAGCCAA 129
QY 69 ValProLysThrGlyGluThrGlnSerThrSerCysPheLysAsnAspAlaAlaIleGly 88
DB 130 GCAGGGAACA---ACGAGCTTACCAACAAGTGTCTTTTCTTAC-----ACTGCAGCA 180
QY 89 AspLeuAsnPheLeuGlyGlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThr 108
DB 181 AATCTTACCTTCTTGGGACGAGATTTCTCTTCAATTTTGACAAATATATTTGCTACT 240
QY 109 AlAserGlyAlaAlaIleGlySerGlnAlaAlaAsnLysThrValThrLeuSerGlyPhe 128
DB 241 GTTGAAGGTGTTGTTTGAACATACAGAGCTTCTGGGATTACCAAAATTTCTCAGGATTT 300
QY 129 SerAlaLeuSerPheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIle 148
DB 301 TCACTCTTCGAGATCTTGCAGCTCTGAGACCA----- 336
QY 149 AsnValLysGlyAsnLeuSerLeuLeuAspAspLysValLeuIleGlnAspAsnPhe 168
DB 336 ----- 336
QY 169 SerThrGlyAspGlyAlaIleAsnLysValGlySerLeuLysIleAlaAsnAsnLys 188
DB 336 ----- 336
QY 189 SerLeuSerPheIleGlyAsnSerSerSerThrArgGlyAlaIleHisThrLysAsn 208
DB 336 ----- 336
QY 209 LeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAla 228
DB 336 ----- 336

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DR WPI; 2000-365569/31.
DR P-PSDB; AA94327.

P-PSDB; AAY94327.

PT Novel Chlamydia 98 kDa putative outer membrane protein antigen, used for vaccination and protection against Chlamydia infection - PT

PS Claim 1; Fig 1; 93pp; English.

The present sequence is the 98kDa putative outer membrane protein gene from *Chlamydia pneumoniae*. The genomic sequence was amplified using two PCR primers. The 5' primer contains a NotI restriction site, a ribosome binding site, an initiation codon and a sequence close to the 5' end of the 98kDa putative outer membrane protein coding sequence. The 3' primer contains the sequence encoding the C-terminal sequence of the putative outer membrane protein and a BamHI restriction site. The stop codon was excluded and an additional nucleotide was inserted to obtain an in-frame C-terminal fusion with the Histidine tag. The PCR product was cloned into a eukaryotic expression vector (pC3-Myc-His) by restricting both the vector and the PCR product with NotI and BamHI and performing a ligation reaction. This expression vector was injected intramembranally and intranasally into mice, which were subsequently inoculated with *Chlamydia pneumoniae*. The chlamydial lung titers of the immunised mice were lower than those of the controls. Thus the 98kDa putative outer membrane protein can be used as a vaccine to provide protective against *Chlamydia* infections, especially *Chlamydia pneumoniae* infections. The polypeptide may also be administered orally to treat *Chlamydia* infection. The present sequence may also be used in the construction of attenuated *Chlamydia* strains that can over-express the gene or express it in a non-toxic form.

SQ Sequence 3000 BP; 871 A; 617 C; 634 G; 878 T; 0 other;

Alignment Scores:

Pred. No.:	7,75e-110	Length:	3700
Score:	1580.50	Matches:	375
Percent Similarity:	52.54	Conservative:	121
Best Local Similarity:	39.72*	Mismatches:	306
Query Match:	36.80*	Indels:	142
DB:	21	Gaps:	19

US-09-830-446-27 (1-841) X AAA27021 (1-3000)

QY 13 ThleuSerMetSerMetLeuLeuGlyAlaAlaThrThrGluGluLeuSerHisSerAsn 34
Db 134 ACATTGGCTATTTTCCCTTGTCTATGATGCTACCGAGACAGTTTGGAATTCAGTGC 193
QY 35 SerPheAspGlyThrThrSerThrThrSerPheSerSeryThrSerSerAlaThrAsp 54
Db 194 AGTTTGATGATGG---AATAAATAATGTAATTTTTCAGTTGCGAGAGTCAGAGAAATGCT 250
QY 55 GlyThrAsnTyrValPheIlyAspSerValValIleGluAsnValProIyThrGlyGlu 74
Db 251 GGAACTCACTCACTATTTTAAAGGAAATGTCACTCAAGAAATATCTCGGAACAGGCACA 310
QY 75 ThrGlnSerThrSerCysPheIlyAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGly 94
Db 311 GCATCAACAAAAAGCTGTTTAAACAC-----ACTAAGGGCGATTTTACCTTCAACAGT 366
QY 95 GlyIlyPheSerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIle 114
Db 365 AACGGGAACCTCTATGTGTTCCAAAGCGGAGATGCAAGGACTGTAGCGAGGCTGCTGTT 424
QY 115 GlySerGluAlaAlaAsnIlyThrValThrLeuSerGlyPheSerGlyLeuSerPheLeu 133
Db 425 AACGCAAGCGCTGTAGTAATATCTACACAGTTTATAGGGTTTCTCCGATCTTTATTT 484
QY 135 LysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValIys---GlyAsn 153
Db 485 GCGTCTCTCGGAAGTTGATGATACACCGGAAAGAGCGCTTAGCGTCAACGGATGAC 544
QY 154 LeuSerLeuLeuAspAsnAspIlyValLeuIleGlnAspAsnPheSerThrGlyAspGly 172
Db 545 TTGAGTTTGACAAAAATGTCAAGTTGCTCTTCACGAAAAACCTTTTCAACGATATATGC 604

Oy	17		GlValAlIleAsnys-----	178
Db	605		GgIcTtATcACCGCAAAAACtTtTcATTAAGAGGACTCAATGTCAGCTCTCTTtTCT	664
Oy	178	----	-----	178
Db	665		GAAMATACtTCTCAAGAAAGGCGAGcATTGACtTCCGATGCCCTTACATTACT	724
Oy	178	----	-----	178
Db	725		GGAACCAAGGGAGTCTCTTTTCTGACAAATCTTCTCGATTCTCGAGCTGCATT	784
Oy	179	----	-AlaGlsertLeuylleAlaAsnAsnLysSerLeuSerPheIle-----	193
Db	785		TTTACAGAGcCTCGGAGcATTtTCTAAATATGCTAAAGtTCTTATATGACATTAAG	844
Oy	193	----	-----	193
Db	845		GTCAcAGAGCGAGcCTCTCAACACGGGGATATGTCAAGAGGTGATCTGCTTAT	904
Oy	194	----	-----Gly	194
Db	905		AAAACtAGTACAGTACTAAGGTACACCTCAGCTGAAATCAGATGTACTTTCAGCAAC	964
Oy	195		AsnSerSerThrArglyGlyValAlIleHlThrLysAsnLeuThrLeuSerSergly	214
Db	965		AATACATGACACACAGCGGGAGGAGCTATCTATGTGAAAAGCTCGAACTGGCTCCGGA	1024
Oy	215		GlyLuhThrLeuPhe-----GlnGlyAsnThrAlaProThrAlaAlagly	229
Db	1025		GGACTTACCCCTATTCAGTAGAATAATGTCAATGAGGTACAGCTCC-----	1072
Oy	230		LysGlyGlyAlAlAlAlAlAlAspSerglyThrLeuSerIleSerglyAspSergly	249
Db	1073		AAAGGTGAGCCATAGCTATCGAAGATATGtGGGAATTAAGCTTATCCGCCGATGTGT	1132
Oy	250		AspIleIlePheGlyAsnThrIleGlyAlaThr-----GlyThrValSerHisSer	267
Db	1133		GACATGTGCTTTTAAAGGAATACAGTCACCTCTCACTCCTCGGAGC--AATAGAAGT	1189
Oy	268		AlAlIleAspLeuGlyThrSerAlaIleThrAlaLeuAlaGlyAlaGlyAlaIleThr	287
Db	1190		AGATACACTTAAGAACAGAGTGCAAAGATGACAGCTTGGCTTCTGCTCGCTGAGACC	1244
Oy	288		IleTyPheTyAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsn	307
Db	1250		ATCTACTCTATGATCCCATTAACACAGATCATCCACACAGTACAGATGTCTTAAAA	1309
Oy	308		IleAsnSerProAspThrGlyAspAsnLysGlyTyThrGlyThrIleValPheSergly	327
Db	1310		GTTAATGAGACTCCGGCAGATTCTGCACCTACAAATATACAGGAACATATCTTACAGGA	1366
Oy	328		GlyLysLeuThrGlyAlaGlyAlaLysAspGlyLysAsnArgThrSerLysLeuLeuGln	347
Db	1370		GAHAAGTATACGACAGACAGGCGCGCAATCTAAATCTTACTTCAGAGCTACTACAG	1422
Oy	348		AsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAlaAsn	367
Db	1430		CCTGTAACTCTTTCAGAGGTACTCTTAAACCTTGAGTGACCTCTGAGACTGAC	1488
Oy	368		GlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeu---Val	386
Db	1490		GCATTCTCAACAGCAGATTTCTGCTTCAAAATGACGTAGAACTACCTTAAACCT	1544
Oy	387		AlaAsnThrGlySerIleGlyLeuThrAsnLeuGlyIleAsnIleAspSerLeuArgAsn	406
Db	1550		GCTGATCTACAGCACAATA-----AACATTTGGTCATTAACTACGATTCATTAACCGT	1603
Oy	407		GlyLysLysIleLysLeuSerAlaAlaThrLagLysAspIleArgIleAspArgPro	426
Db	1604		GCAAGAGGCAAAATATGAACCAACAGCTACGTAAATAATCTGACTTTATCTGAAAC	1666

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QY 427 ValValLeuAlaIleSerAepGluSerPheTyrGlnaAnglyPheLeuAangluAaspHis 446
   ::::::::::::::::::::
DB 1664 ATCACTTATTGGACCCGACGGGACCTTTATGAAATCATAGTTTAAGAAATTCCTCAG 1723
QY 447 SerTyrAapGlyIleLeuGluLeuAapAlaGlyIyAaapIleValIleSerAla--Aasp 466
   |||||
DB 1724 TCCACACAC--ATCTTAAGAGCTCAAGAGCTTCGGAACGTGAACMACACCGCAGTACT 1780
QY 466 eArYSerIleAapAlaValGlnSerPro--TyrGlyTyrGlnIlySerTP---ThrIle 484
   ::::::::::::::::::::
DB 1781 CCGAGTCTTAATAGGTGTAGGAAATTCATTAACGGCTATACGGGACCTTGCGGCCCAAT 1840
QY 485 AasnTyrSerThraP--AaplyblyAalAthrValSerTrrAlaYsgInSerPheasn 503
   |||||
DB 1841 GTTGGGGGACAGGGGCTTCAACAGCTCAACCTTCAACTGAATAAAGCTGGCTAATAT 1900
QY 504 ProThraIaGluGlnGluAlaProLeuValProAasnLeuLeuTrrGlySerPheIleAap 523
   |||||
DB 1901 CCTAATCCCGAGGGTATCGGCTCTTATGCTCTTAATAGCTTAATGAATGATTAATAGAT 1960
QY 524 ValArgSerPheGlnAepHeilIeGluLeuGlyThrgluGluAlaProTrrGlyIlyArg 543
   ::::::::::::::::::::
DB 1961 ATTAGCTCTTCCATTAATCTTAATGAGACTGCAACGAAAGGGTTCAGGAGACCGTCT 2020
QY 544 PheTrrValaIaGlyIleSerAasnValIleuHisArgSerGlyArgGluAangluArgLys 563
   |||||
DB 2021 TTTTGGTGCTGATATCTTAATCTTCCATTAAGAGTAGTCAAAABAACAGACGGCGG 2080
QY 564 PheArgHisValSerGlyGlyAlaValGlyIlyAaSerThraArgMetProGlyGlyAap 583
   |||||
DB 2081 TTTTCGCATTTGAGTGCGGCTTATGTCATAGAGAAACCTACATCTTTCAGATTAAG 2140
QY 584 ThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAapIlyArgPheMetAanThr 603
   |||||
DB 2141 ATTCTTAGTCTGCTGATTTTGTACGCTTTGAGAAAGATAGAGCTAATCTTGTAGCTAAG 2200
QY 604 AasnPheAlaIyAsthTrrAlaGlySerLeuArgLeuGlnHisAapAlaSerLeuTrrSer 623
   |||||
DB 2201 AATCAAGATACAGCTACGAGGAACTCTTAATTAACAGACAAAGAACTTAATCTCT 2260
QY 624 ValValSerIleLeuLeuGlyGlyGlyIlyLeuArgGluIleLeuLeuProTrrValSer 643
   ::::::::::::::::::::
DB 2261 CTTCCTTGC-----AAACTACGGCTTGTCTGTTGCTTATGTTCTCT 2302
QY 644 LysThrLeuSerProCysSerPheTrrGlyGlnLeuSerTrrGlyHisThrAapHisAagMet 663
   |||||
DB 2303 ACAGAGATTCCTGTTCTCTTTACGAAACCTTAGCTACCCATACGAGATTAACGATCTG 2362
QY 664 LysThrGlnSerLeuProProProProProThrLeuSerThraAapHisThrSerTrrGly 683
   |||||
DB 2363 AAAACCAAGAT-----ACAACATATCTCTGTTAAAGAAAGCTGGGGG 2407
QY 684 GlyTrrValTrrAlaGlyGluLeuGlyThraArg-----ValAlaValGlnAanThrSer 701
   ::::::::::::::::::::
DB 2408 AATGATAGTTTCCCTTTAGAAATTCGGTGAAGAGCTCCGATTGCTTAGATGAAGAGTCT 2467
QY 702 GlyArgGlyPhePheGlnGluTrrThrProPheValIyValGlnAlaValIlyTrrAlaArg 721
   |||||
DB 2468 -----CTATTGACGATACATGCTCTTAAGAAATTTGAGATTTGCTTATGACAT 2518
QY 722 GlnAapSerPheValGluLeuGlyAlaIleSerArgAapPheSerAapSerHisLeuTrr 741
   |||||
DB 2519 CAGGAAGGTTTAAAGAACGGAACGAAAGCTCTGTAATTTGGAAAGTACCGCTTTGTCG 2578
QY 742 AasnLeuAlaIleProLeuGlyIlyIyValLeuGluIlyArg-----PheAlaGluGlnTrr 759
   |||||
DB 2579 AATCTTGCTTACCTTACCTTACCGGATCCGATTGATTAAGAAATCAGACTGCCAAAGTCAAG 2638
QY 760 TrrHisValValAlaMetTrrSerProAapValCysArgSerAapProLysCysTrrThr 779
   |||||
DB 2639 TACAACTTAACCTTGGTTTATACCTGAGATCTTGTCTGTAAGTAAACCCGACTGTAGACA 2698
QY 780 ThrLeuLeuSerAangluGlySerTrrPlyThrIyGlySerAasnLeuAlaArgGlnAla 799

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DB 2699 ACACTGCAATTAGCCGTGATCTTGAAAAACCTTCGGTACGAATTTGGCAACAAGCT 2758
QY 800 GlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaIaGluLeuPheGlyAasn 819
   ::::::::::::::::::::
DB 2759 TTAGTCTTCGTGACAGGAACCAATTTTGCTTAACCTCAAAATTTTAAGCTTTAGCCAA 2818
QY 820 PheGlyPheGlyTrrPargIySerSerArgSerTrrAasnValAapAlaGlySerIlyIle 839
   |||||
DB 2819 TTTTCTTTGAATTCGTGGTGTATCTCGCAATTAACAATGTAACCTTAAGAGCAAAATAC 2878
QY 840 LysPhe 841
   |||||
DB 2879 CAATTC 2884

RESULT 8
ID AAX06820 standard; DNA; 2787 BP.
XX AAX06820;
AC AAX06820;
DT 26-APR-1999 (first entry)
DE Chlamydia pneumoniae surface exposed protein Omp8 DNA.
XX
XX Omp8; outer membrane protein 8; surface exposed protein; antigen;
KM infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
XX
XX Chlamydia pneumoniae.
XX
XX W09858953-A2.
PD 30-DEC-1998.
XX
XX 19-JUN-1998; 98MO-DK00266.
PR 23-JUN-1997; 97DK-0000744.
PA (BIRK/) BIRKELUND S.
PA (CHR/) CHRISTIANSEN G.
PI Birkelund S, Christiansen G, Knudsen K, Madsen A;
PI Mygind P;
XX
DR WPI, 1999-105610/09.
DR P-PSDB; AAM88421.
XX
XX Species-specific test for identifying mammals infected with
PT Chlamydia pneumoniae - comprises detecting antibodies specific for
PT outer membrane proteins of C. pneumoniae or nucleic acids encoding
PT these proteins
XX
PS claim 6; Page 52-53; 115pp; English.
XX
XX This DNA sequence codes for the novel 90.0 kDa surface exposed
CC protein Omp8 (see AAM88421) of the human respiratory pathogen
CC Chlamydia pneumoniae. By generating antibodies against C.
CC pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
CC was obtained which reacted with outer membrane proteins. The
CC antibody was used to identify the genes (see AAX06816-27) encoding
CC Omp4-Omp15 proteins (see AAM88417-28) in an expression library of
CC C. pneumoniae DNA. The genes are situated in 2 gene clusters;
CC Omp11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
CC the other, and encode polypeptides of about 89.8-100.3 kDa and
CC about 56.1 kDa. The invention provides a new species specific test
CC for identifying mammals (including humans) infected with Chlamydia
CC pneumoniae. The test comprises detecting antibodies specific for
CC Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
CC membrane proteins, especially by PCR. The proteins are also used
CC in the diagnosis of C. pneumoniae infection in mammals. The
CC nucleic acids and proteins can also be used in the immunization of
CC mammals, the nucleic acids being particularly useful as DNA
CC vaccines for effecting in vivo expression of antigens. The

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CC vaccines may also prevent atherosclerosis and bronchial asthma,
CC which are possibly associated with *C. pneumoniae*.

XX Sequence 2787 BP; 811 A; 583 C; 598 G; 795 T; 0 other;

Alignment Scores:

Pred. No.:	4,79e-109	Length:	2787
Score:	1569.50	Matches:	373
Percent Similarity:	52.33%	Conservative:	121
Best Local Similarity:	39.51%	Mismatches:	308
Query Match:	36.54%	Indels:	142
DB:	20	Gaps:	19

US-09-830-446-27 (1-841) x AAX06820 (1-2787)

```

QY 15 ThrLeuSerMetSerAsnLeuGlyAlaIaThrGluGluLeuSerAlaSerAsn 34
DB      :::::
DB 34 ACATTGCTATTTCCTTGTCTATGATGCTACCGACAGATTGGATTCAAGTCG 93
QY 35 SerPheAspGlyThrThrSerThrThrSerPheSerSerThrThrSerAlaThrAsp 54
DB 94 AATTTCGATGCG---AATATAAATGTAATTTTTCAGTTCTGAGAGTCAGAAAGATGCT 150
QY 55 GlyThrAsnThrValPheLeuAspSerValIleGluAsnValProlySerThrGlyGlu 74
DB 151 GGAATCTACTACTATTAAAGGAAATGTCATCTAAGAAATATTCCTCGAACAGGACACA 210
QY 75 ThrGlnSerThrSerGlyPheLeuAsnAspAlaIleGlyAspLeuAsnPheLeuGly 94
DB 211 GCATCTCAAAAGCGTGTTTTAAACAC-----ACTAAGGCGCATTTGACTTTCACAGCT 264
QY 95 GlyGlyPheSerPheThrPheSerAsnIleAspAlaIaThrThrAlaSerGlyAlaIle 114
DB 265 AACGGGAACCTCTTATTGTTTCCAAACGGGATGCGACGATGACAGGCGCTGTGTT 324
QY 115 GlySerGluAlaIleAsnThrValThrLeuSerGlyPheSerAlaLeuSerPheLeu 134
DB 325 AACAGCAGCGGTGGTAAATATCTACACAGTTTATAGGGTTTCTTCGCTATCTTTATT 384
QY 135 LysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValIys---GlyAsn 153
DB 385 GCGTCTCCGGAAGTTCGATTAACCGGCAAGGCGGTGAGCTCTCAACGGATATGCG 444
QY 154 LeuSerLeuLeuAspAsnAspLeuValIleGluAspAsnPheSerThrGlyAspGly 173
DB 445 TTGAATTTGACAAAAATGTCAAGTTGCTCTTCAGCAAAACTTTTCAACGGAATATGCG 504
QY 174 GlyAlaIleAsnCys----- 178
DB 505 GGTGCTATCACCGCAAAAATCTTTTCAATTACAGGATCAATGTCAGCTGTGTTTCT 564
QY 178 ----- 178
DB 565 GAAATATCTCTCTCAAGAAAGGCGAGCCATTGACATTCGATCCCTTACATTACT 624
QY 178 ----- 178
DB 625 GGAACCAAGGGAGATCTTTTCTGACATATCTTCTCGAGTTCTGAGCTGCATTT 684
QY 179 -----AlaGlySerLeuLysIleAlaAsnAsnLysSerLeuSerPheIle----- 193
DB 685 TTTCAGAAAGCCCTCGGTGACTATTTCTAATATGCTAAAGTTCTTTATTCACATAAG 744
QY 193 ----- 193
DB 745 GTTCACAGAGCAGCTCTCAACACGCGGATATGTCAGAGTGTCTATCTGTCTTAT 804
QY 194 -----Gly 194
DB 805 AAAACTATGACATCTAAGTACACCTCTCACTGGAATTCAGATGTTACTTTCAGCAAC 864
QY 195 AamSerSerSerThrArgGlyGlyAlaIleLysThrLysAsnLeuThrLeuSerSerGly 214
DB      :::::

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DB 865 AATACATGACAAACGCGGAGAGCTATCTATGTGAAAGAAAGCTGAACTGCTCCGGA 924
QY 215 GlyGluThrLeuPhe-----GlnGlyAsnThrAlaProThrAlaIleGly 229
DB 925 GCACTTACCCTTATTCAGTAAGAAATATGCTCAATGAGGTACAGCTCTC----- 972
QY 230 LysGlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSerGly 249
DB 973 AAAGGTGAGGACATGCTATTCGAAGATATGAGGAAATGAGTTTATCCGCGATGTGCT 1032
QY 250 AspIleIlePheGluGlyAsnThrIleGlyAlaThr-----GlyThrValSerHisSer 267
DB 1033 GACATGTCTTTTATGGAATACAGTCACTTCTACTCTCCGAGAC---AATGAAGT 1089
QY 268 AlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuAlaGlnGlyHisThr 287
DB 1090 AGTATGACTTATAGGAACAGATGCAAAAGATGACAGCTTTCGCTGCTGTGAGACC 1149
QY 288 IleThrPheThrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsn 307
DB 1150 ATCTACTTCTATGATCCCATATCTACAGATCTTCCACACAGCTTACAGATGCTTAAA 1209
QY 308 IleAsnSerProAspThrGlyAspAsnLysGlyThrGlyThrIleValPheSerGly 327
DB 1210 GTTATGAGACTCCGCGACAGATTCTGACTACATATACAGGGAACATCATCTTACAGGA 1269
QY 328 GlyLysLeuThrGluAlaGluAlaLysAspGlyLysAsnAsnThrSerLysLeuGln 347
DB 1270 GAAAAGTATATCAGACACAGAGCGCGACATTTTAAAAATCTTACTTCGAAAGCTTACAG 1329
QY 348 AsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAlaAsn 367
DB 1330 CCTGTACTCTTTCAGAGAGTACTATCTTAAACATGAGATGACTCTGACAGCTCAG 1389
QY 368 GlyPheSerGlnAspAlaAsnSerLysLeuIleLysAspLeuGlyThrSerLeu---Val 386
DB 1390 GCATCTCACTCAACAGGCGAGATTCTGCTCGAAATGAGCGTACGAACTTACAGACT 1449
QY 387 AlaAsnThrGlnSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuAsn 406
DB 1450 GGTGATCTACGACCATAT-----AACATTTGTCATTAAACATGATGTTATTAACGCT 1503
QY 407 GlyLysLysIleLysLeuSerAlaIleAlaThrAlaGlnLysAspIleArgIleAspArgPro 426
DB 1504 GCAAAAGAGCGCAAAATATGAACCAAGCTACGTCGAAATTAATCTGACTTATCTGGAAC 1563
QY 427 ValValLeuAlaIleSerAspLysSerPheThrGlyAsnGlyPheLeuAsnGluAspHis 446
DB 1564 ATCACTTATTGACCCGACCGGCGACGTTTATGAAATCATATGTTAAGAAATCTCAG 1623
QY 447 SerThrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleValIleSerAla---AspS 466
DB 1624 TCTTACGAC---ATCTTAGAGCTCAAAAGCTCTCGAACGTGAACAAGCACCGCATGCT 1680
QY 466 AsnSerSerIleAspAlaValGlnSerPro---TyrGlyThrGlnGlyLysTrp---ThrIle 484
DB 1681 CCAAGTCTCTATATATGGGTGAAGAAATTCATTACGCTTACAGGAACTTGGGCGCCATTT 1740
QY 485 AsnTrpSerThrAsp---AspLysLysAlaThrValSerTrpAlaLysGlnSerPheAsn 503
DB 1741 GTTGGGGGACAGGGGCTTCTACAGACTCAACCTTCACTGGAATAAACTGGCTATATT 1800
QY 504 ProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySerPheIleAsp 523
DB 1801 CCTAATCCGAGCGTATGCGCTCTTATGCTCTTAATACCTTATGGAATGATCATTTATGAT 1860
QY 524 ValArgSerPheGlnAsnPheIleGluLeuGlyThrGlnGlyAlaProGlyLysArg 543
DB 1861 ATTACTCTCTCCATATCTTATGAGAGCTGCAACGAAAGGTTCCAGAGAACCTGTCT 1920
QY 544 PheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyLysGluAsnGlnArgLys 563
DB 1921 TTTTGTTGCTGCTATCTTAACTTCTTCAATAGATAGTAAACAAACAGACGCGGG 1980

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QY 564 PheArgHisValSerGlyGlyAlaValAlaGlyAlaSerThrArgMetProGlyGlyAsp 563
 DB 1981 TTTCGGCATTTGAGTGGCGGTATGTCATAGAGAAACCTACATCTTGTCAAGTAA 2040
 QY 584 ThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspIleAspTyrPheMetAsnThr 603
 DB 2041 ATTCTTAGAGCTGCATTTTGTCTCTTTCAGAGAAAGATGAGACTACTTGTAGCTTAA 2100
 QY 604 AsnPheAlaIleThrTyrAlaGlySerLeuArgGlnHisAspIleAsnLeuTyrSer 623
 DB 2101 AATCAAGGTACAGTCTACGAGAGAACTCTATTATACGACAAACCAATATCTCT 2160
 QY 624 ValValSerIleLeuLeuGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 643
 DB 2161 CTTCCTTGC-----AACTACGGCCTTGTCTGTCTTATGTTCTT 2202
 QY 644 LysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAspHisArgMet 663
 DB 2203 ACAGAGATTCCTGTTCTCTTTCAGAGAAACCTTAGCTACACCATACGAGTAAAGATCTG 2262
 QY 664 LysThrGluSerLeuProProProProProThrLeuSerThrAspHisThrSerTyrGly 683
 DB 2263 AAAACCAAGTAT-----ACAACATATCTCTTAAAGAACTGGGG 2307
 QY 684 GlyTyrValTyrAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 701
 DB 2308 AATGATGATTCCTGCTTAGAATTCGGTGAAGAGCTCCGATTTGCTTAGATGAAGTCT 2367
 QY 702 GlyArgGlyPhePheGlnGlyTyrThrProPheValIleValAlaValTyrAlaArg 721
 DB 2368 -----CTATTGAGCAGTACATGCCCTCATGAAATTCGAGTTGTCTATGACAT 2418
 QY 722 GlnAspSerPheValGlyLeuGlyAlaIleSerArgAspPheSerAspSerHisLeuTyr 741
 DB 2419 CAGGAAGGTTTAAAGAACGAGAACAGAGCTCGTAATTTGAAAGTACCGCTTGTG 2478
 QY 742 AsnLeuAlaIleProLeuGlyIleLeuGlyLeuArg-----PheAlaGlnGlnTyr 759
 DB 2479 AATCTTGCCTTACTATCCGGATCCGATTTGATAGAAACACAGCTCCAAAGTCAAG 2538
 QY 760 TyrHisValAlaIleMetTyrSerProAspValCysArgSerAsnProIleCysThrThr 779
 DB 2539 TACAACTAACTCTGTTGTTATACGTGAGACTTGTCTGTAGTAAACCCGACTGACGACA 2598
 QY 780 ThrLeuSerAsnGlnGlySerTyrPheThrIleGlySerLeuAlaArgGlnAla 799
 DB 2599 ACACTCGAATTAGCCGTGATCTTGAAAACTTCGGTACGAATTTGGCAACAGACT 2658
 QY 800 GlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaIleGlyLeuPheGlyAsn 819
 DB 2659 TTAGTCTCTCGTCAGAGAAACATTTTGTCTTAACCAATTTTGAAGCTTTAGCCAA 2718
 QY 820 PheGlyPheGlyIleTyrArgGlySerSerArgSerTyrAsnValAlaIleGlySerIle 839
 DB 2719 TTTTCTTTGAATTGCGTGGTCACTCCGCAATTACAGTGTAGCTTAGAGAGCAAAATAC 2778
 QY 840 LysPhe 841
 DB 2779 CAATTC 2784
 Db 2779 CAATTC 2784
 RESULT 9
 ID ABQ84758 standard; DNA; 2520 BP.
 XX ABQ84758;
 AC ABQ84758;
 DT 25-FEB-2003 (first entry)
 XX Chlamydia psittaci antigen CP4#4 encoding DNA SEQ ID NO:22.
 DE Chlamydia psittaci; vaccination; vaccine; antigen; immune response;
 KW immunisation; antibacterial; infection; gene; ds.

XX OS Chlamydia psittaci.
 XX FH Key Location/Qualifiers
 FT CDS 1..2520
 FT /tag= a
 FT /product= "antigen CP4#4"
 PN MO200253588-A2.
 XX PD 11-JUL-2002.
 XX PF 17-DEC-2001; 2001MO-US48715.
 XX PR 15-DEC-2000; 2000US-0738269.
 XX PA (TEXA) UNIV TEXAS SYSTEM.
 XX PI Johnston SA, Stenke-Hale K, Sykes KF, Kaltenboeck B;
 XX PI WPI: 2002-537942/57.
 DR P-PSDB; ABP56002.
 XX PT Vaccine for immunization of animal, preferably bovine, against
 PT Chlamydia psittaci, comprises at least one polynucleotide having a C.
 PT psittaci sequence, or at least one C. psittaci antigen
 XX PS Claim 14, Page 126; 164pp; English.
 CC The present invention describes a vaccine (I) for the immunisation of an
 CC animal against Chlamydia psittaci comprising at least one polynucleotide
 CC (Ia) having a C. psittaci sequence, or at least one C. psittaci antigen
 CC (Ib), and a carrier. (Ia) and (Ib) have antibacterial activity. (I) is
 CC useful for the immunisation of a bovine. The present sequence encodes a
 CC C. psittaci antigen from the present invention.
 SQ Sequence 2520 BP; 774 A; 584 C; 490 G; 672 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 1,29e-103 Length: 2520
 Score: 1497.00 Matches: 357
 Percent Similarity: 56.21% Conservative: 132
 Best Local Similarity: 41.03% Mismatches: 321
 Query Match: 34.85% Indels: 60
 DB: 24 Gaps: 25
 US-09-830-446-27 (1-841) x ABQ84758 (1-2520)
 QY 1 MetIleIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
 DB 1 ATGAACATCCAGTCTACTGTTCTTAATATCC-----TCAGCCTATTGGCTGAAT 54
 QY 21 LeuLeuGlyAlaAlaThrThrGluGlu-----IleSerAlaSerAsnSerPheAspGly 38
 DB 55 TCTTTAGCTCGCTACACAGCGCTCAACAGCCTTAATCCCTCCGATGACTAATGGA 114
 QY 39 ThrThrSerThrThrSerPheSerSerIleThrSerSerAlaThrAspGlyThrAsnTyr 58
 DB 115 AATGTACCTCTGAGAGAGTTCCAGGTAAAGAAATTCATCA-----GGAACACGTAAT 168
 QY 59 ValPheLysAspSerValAlaIleGluAsnValProLysThrIleGlyLunThrGlnSerThr 78
 DB 169 ACTTGGAAAGCAATGTGTATCTCTTTCAGAGAGAAAGATTCAAGTCTAAAGAAA--- 225
 QY 79 SerCysPheLysAsnAlaAlaIleGlyAspLeuAsnPheLeuGlyGlyGlyPheSer 98
 DB 226 AGTTGTTTC-----TCAGCTACTGATTAACCTTACCTCTTAGAGAAACGGGTATACT 276
 QY 99 PheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGlyAla 118
 DB 277 CTTCCTTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 336
 QY 119 AlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAla 138

Db 337 CAAGGAAAACCTTAGCATCTCAGAGATTCTTATTTTCATGTCCTTATGTCCTCA 396
 Qy 139 SerThrValThrAsnGlyLeuGlyValAlaIleAsnVallyrGlyAsnLeuSerLeuLeuAsp 158
 Db 397 GGC-----ACAACTGGATTACGAGACTATACAGACTAAAGGCACAACTTAAAGAAAT 450
 Qy 159 AsnAspLyValLeuIleGlnAspAsnPhSerThrGlyAspGlyGlyAlaIleAsnCys 178
 Db 451 AACTCTAATCTTGTCTTCCATTAATAAAGCTCTCAACAGCAAGAAAGGTGGGCTTTCAGAGT 510
 Qy 179 AlaGlySer-----LeuLyValIleAsnAsnLySerLeuSerPheIleGly 194
 Db 511 AAAGGAGCAGATGATGCTGAATTAAATAAGAAATAATACAGAACTGCTTTTCTCAGAA 570
 Qy 195 AsnSerSerSerThrArgGlyGlyAlaIleHisThrLyAsnLeuThrLeuSerSerGly 214
 Db 571 AACTCTCTCAGCTCAAAAGCGGGCTATTTATGCTGATTAACCTCAACCATGCTCAGGT 630
 Qy 215 GlyIuThrLeuPheGlnGlyAsnThrAlaProThrAlaAlaGly---LyGlyGlyAla 233
 Db 631 GGGCTCACTATTTTCTTAAACACTCTGTATCCAAAGGTTCAATCCCTTAAAGCGGAGCT 690
 Qy 234 IleAlaIleAlaAsp---SerGlyThrLeuSerIleSerGlyAspSerGlyAspIleIle 252
 Db 691 ATTGACATTAAGATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 750
 Qy 253 PheGlnGlyAsn-----ThrIleGlyAlaThrGlyThrValSerHisSerAla 268
 Db 751 TTCGATGGGAACAAATCATCAAACTAGTGTGATGATGATGATGATGATGATGATGATGAT 810
 Qy 269 IleAspLeuGlyThrSerAlaLySerIleThrAlaLeuArgAlaAlaGlnGlyHisThrIle 288
 Db 811 ATGATCTCGGACAC---GGAAATTTACAAAGCTACGCTTAAAGCGGCTTCGAAAT 867
 Qy 289 TyrPheTyAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsnIle 308
 Db 868 TTCTCTATGACCTTATTAAGCTGCGGAGAGATCT-----GATGAATCAAACTT 915
 Qy 309 AsnSerProAspThrGlyAspAsnLyGlyGlyThrGlyThrIleValPheSerGlyGly 328
 Db 916 AATAAATAAAGAAAGCTGTGAT-----TATACAGAAAGATGCTCTTCTCAGGTCAA 966
 Qy 329 LysLeuThrGluAlaGluAlaLyAspGlyLyAspAsnArgThrSerLyLeuLeuGlnAsn 348
 Db 967 AATTTATTCGATGAAGAAAGAAAGCAAGCGGAAACCTAGCTTCACTTCAACCAACCC 1026
 Qy 349 ValAlaPheLyAsnGlyThrValAlaLeuLyGlyAspValValLeuSerAlaAsnGly 368
 Db 1027 ATCAATTAATACGAGATCTCTGTTACTTAAAGATGGTATCTGTAAACGCAAAACA 1086
 Qy 369 PheSerGlnAspAlaAsnSerLyLeuIleMetAspLeuGlyThrSerLeu----- 385
 Db 1087 GTAAGCGCAAGAAAGCGGATCTACCGTTCATGATGATGATGATGATGATGATGATGAT 1146
 Qy 386 ValAlaAsnThrGlnSerIleGluLeuThrAsnLeuGlnIleAsnIleAspSerLeuArg 405
 Db 1147 TCTTAGGTCGAGAAACATCAACCTTAATATCTAGATATTAACATGCGCTGTTGGGG 1206
 Qy 406 AsnGly-----LyLyValIleLeuSerAlaAlaThrAlaGlnLyAspIleArg 422
 Db 1207 GGGGGGGGGGGGATCCTCTCTGCTAAACTCGCAACAATACAGCAAGTCAAGCTTAATCT 1266
 Qy 423 IleAspArgProValValLeuAlaIleSerAspGlySerPheTyGlnAsnGlyPheLeu 442
 Db 1267 ATTAAC---GCTGTCAATCTAGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1323
 Qy 443 AsnGluAspHisSerTyAspGlyLyIleGlnIleuLeuAspAlaGlyLyAspIleValIle 462
 Db 1324 GGTAGCTTAAACCTTTCACAGCAATAGTACCTAACAAGCTAAGCTAAGTCAACAG 1383
 Qy 463 SerAlaAspSerArgSerIleAspAlaValGlnSerProTyGlyTyGlnGlyLyAspTyr 482

Db 1384 CTTACAGATATCTACAAATTAATGCTCTCTACTCATTAACGTTACCAAGAAATGG 1443
 Qy 483 ThrIleAsnTrpSerThrAsp-----AspLyLyValAlaThrValSerTrpAlaLyGln 500
 Db 1444 ACAGTACTTGGGACACCGAAACAGCTACAAATAACAGCCACTTAACCTTGGGAACAACT 1503
 Qy 501 SerPheAsnProThrAlaGlnGlnIleAlaProLeuValProAsnLeuLeuTrpGlySer 520
 Db 1504 GGTACTCTCCCTTAAACCAAGAAAGCTCAAGAGACCTTATGCTCCGAATACTCTTGGGGTCA 1563
 Qy 521 PheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGlnGlyAlaProTy 540
 Db 1564 TTCTCTACCTCAGAGCTTATCAAACTTAATGATATTAAGCTTAAAGGCGGCTGACTAC 1623
 Qy 541 GlyLyAspPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArgGluAsn 560
 Db 1624 CATAGAGCTTTTGGGATCCGGTCTAGTACTCTTACCAAAAGTGGCTCGATACT 1683
 Qy 561 GlnArgLyAspPheArgHisValSerGlyValAlaValAlaGlyAlaSerThrArgMetPro 580
 Db 1684 AAACGCAAGTTCCGTCAACATAGCGCGGATAGCGCTTAAAGCGTACGCAAAACCTCT 1743
 Qy 581 GlyLyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLyAspTyPhe 600
 Db 1744 TCTGATGATATTTCAATGCGGCTTCTGCGCACTCTCGGAAAGGACAAAGACTATTTA 1803
 Qy 601 MetAsnThrAsnPheAlaLySerThrTyAlaGlySerLeuArgLeuGlnHisAspAlaSer 620
 Db 1804 GTGTGCAAAACCAAGCCACATTTAGCAGGTCTCTATTAATCAAGCA---ATCTCC 1860
 Qy 621 LeuTySerValAlaSerIleLeuLeuGlyGlyGlyLeuArgGluIleLeuLeuPro 640
 Db 1861 TATTTGAC-----GCTTGGCAAGATCTGCTCAAAAC 1893
 Qy 641 TyrValSerLyThrLeuProCysSerPheTyGlyGlnLeuSerTyGlyHisThrAsp 660
 Db 1894 ACTATCGGTGCAAGAGCTCGTATGCTTAAACCAAGATTAATGTCATGCTTCA 1953
 Qy 661 HisArgMetLySerGlu-----SerLeuProProProProThrLeuSerThr 677
 Db 1954 AACGACATGAAGAAACCAATGACATGATCACTTACCTCTCGTAAACCACTATGCGAA 2013
 Qy 678 AspHisThrSerTrpGlyGlyTyThrValTrpAlaGlyGlnLeuGlyThrArgValAlaVal 697
 Db 2014 ATCAAGGATGATGGGATGACATGTTTGGAGTCCAGCTTGGCAACGTGCTCATC 2073
 Qy 698 GluAsnThrSerGlyArgGlyPhePheGlnGlyTyThrProPheValLyValGlnAla 717
 Db 2074 CAACAGATCTCTCTC---CTATTGATATGATCACTCACTTCTCGAAGCTTCAACTT 2130
 Qy 718 ValTyAlaArgGlnAspSerPheValGluLeuGlyAla---IleSerArgAspPheSer 736
 Db 2131 GTGATACGCAACAAGATGACTTAAGGAAACAAATAGCGATCAGGAAAGTACTTGAA 2190
 Qy 737 AspSerHisLeuTyAsnLeuAlaIleProLeuGlyIleLyLeuGluLyArgPheAla 756
 Db 2191 AGCAGCAATCTCACCAACCTTCTCTGCTATCGGATCAAGTTGAG---AGATTGCT 2247
 Qy 757 GluGln-----TyTyHisValAlaAlaMetTySerProAspValCysArgSer 773
 Db 2248 AACAAAGATACAGCTTCTTATCATGCTCACTGCTCTTATCTCTCGATATGTAAAGAGT 2307
 Qy 774 AsnProLySerThrThrThrLeuLeuSerAsnGlnGlySer-----TrpLySerThrLy 791
 Db 2308 AACCTGACTGATCTCTCTCTGTAGTAAAGCCCACTGCTGCTGTGGGTAACGAA 2367
 Qy 792 GlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGly 811
 Db 2368 GCCAAACACTTGGCGCAAGGCGCTTCACTCAAGAGGAAACTACTTCTTTAAGT 2427
 Qy 812 AlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTyTrpArgGlySerSerArgSerTy 831
 Db 2428 CACAACATAGAAATCTTCAGCGAGTTCGTTGAGCTCAGGGGATCTTCAAGAACCTAT 2487


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QY      832 AsnValAspAlaGlySerLysIleLeuPhe      841
          |||||
Db      2488 AACGTAGATCTCGATCGAAGATCCAGTTC      2517
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Db      1147 TCTTCAGGAGGAGAAACATCCCTTAACATATGATTAATTAACATGCGCTGTTGGGG 1206
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      406 Aengly-----LysLysLysLysLysLysLysLysLysLysLysLysLysLys 422
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      1207 GGGGGGGGGGAGTACTCTCTGCTAACTCGCAACAAATACGCAAGCAAGCTTAATCT 1266
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      423 IleAapGProValValLysLysLysLysLysLysLysLysLysLysLysLysLys 442
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      1267 ATTAACT---GCTGTAATCTAGTCAATGCTGAGCAATGCTTAAGAAATCTTAATCTT 1323
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      443 AengLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 462
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      1324 GCTAGCTGTAACCTTTCACAGCAATAGTACAACTAACGTAAGTACAGTACAGG 1383
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      463 SerLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 482
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      1384 CCTACAGTAATCTAACAATATATGCTCTCTACTATACGCTTACCAAGAAATTTGG 1443
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      483 ThrLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 500
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      1444 ACAATACCTTGGAGACCGCAACAGCTACAAACAGCACTCTAACCTTGGCAAACT 1503
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      501 SerPheAenProThrAlaGlnGlnLysLysLysLysLysLysLysLysLysLysLys 520
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      1504 GGCTACTCCCTTAACCCAGAACTGCAAGGACCTTAAGTCCGAAATCTTTGGGGTGA 1563
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      521 PheLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 540
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      1564 TTCTGACCTCAGACTATACAAACCTTAATGCAATATAGGCTCAATGCGCTGACTAC 1623
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      541 GlnLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 560
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      1624 CATAGAGTTTGGATCCGCTAGCTAGTAACTTCTTAACAACAGTGGCTTAATCT 1683
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      561 GlnLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 580
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      1684 AAACCGAAGTTCCGTACAAATAGCCGCGGATAGCTTAAGGCTGACCAAAACTCT 1743
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      581 GlnLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 600
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      1744 TCTGATGATATTTCACTGCGCTTCTGCAACTCTTGGCAAGCAACAAATCTTTA 1803
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      601 MetAenThrAsnPheAlaLysLysLysLysLysLysLysLysLysLysLysLysLys 620
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      1804 GTGTGAAAACAAAGCCCAACTTAAGGAGGTTCTCTATTAATGAGAT---ATCTCC 1860
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      621 LeuTyrSerValValSerLysLysLysLysLysLysLysLysLysLysLysLys 640
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      1861 TATGGAGC-----GCTTGGCAAGATGCTTACAAAC 1893
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      641 TyrValSerLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 660
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      1894 ACTATCGGTGCAAGAGCTCGTTAGTCTTAAGCAAGCACTTAATATGTCATGCTTCA 1953
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      661 HisArgMetLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 677
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      1954 AAGGACATGAAACCAACATGACGACTTACGCTCTCGTAAACAAAGATGAGAA 2013
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      678 AsnHisLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 697
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      2014 ATCAAGGGGTGATGGGTGAAAGTTGTTGAGAGTGAAGCTTGGTGAAGCTGCTATC 2073
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      698 GlnAenThrSerGlyAlaGlyPhePheGlnGlyTyrThrProPheValLysValGln 717
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      2074 CAACAGATCTTCTCTC---CTATTGATATGATCTCACTTTCGAAAGTTCAACT 2130
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      718 ValTyrAlaLysGlyAspSerPheValGlnLysLysLysLysLysLysLysLysLys 736
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      2131 GTGCAATCCGACCAATGATCTTAAGAAACAAATAGGATCAGGAAAGATTACTTGA 2190
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      737 AspSerHisLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 756
      ||:||||| ||:||||| ||:||||| ||:|||||

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Db      2191 AGCAGCATCTCACCAACTTCTCTGCTATCGGCAATCAAGTTTGA---AGATTGCT 2247
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      757 GlnGln-----TyrTyrHisValValAlaMetTyrSerProAspValCysArgSer 773
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      2248 AACACGATACAGCTTCTTAATCATGTCATGCTCTTAATTTCTCGATATGTGAAGAT 2307
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      774 AsnProLysCysThrThrThrLysLysLysLysLysLysLysLysLysLysLysLys 791
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      2308 AACCTGACTTACTACTCTCTCTGTAAGCCCACTGCTGCTGCTGCTGCTGCTGCTGCT 2367
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      792 GlycerAenLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 811
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      2368 GCCAAACACTTGGCGGAGGCGCTTCAATGACAGCAAGAACTACTTCTTTAAGT 2427
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      812 AlaAlaAlaGlnLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 831
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      2428 CACAAATAGAAATCTTACGCCAGTCCGTTTCAAGCTCAGGAGATCTTCAAGAACTAT 2487
      ||:||||| ||:||||| ||:||||| ||:|||||
Qy      832 AsnValAspAlaGlySerLysLysLysLysLysLysLysLysLysLysLysLys 841
      ||:||||| ||:||||| ||:||||| ||:|||||
Db      2488 AACGTAGATCTCGATCGAATCGAATCCAGTTT 2517
      ||:||||| ||:||||| ||:||||| ||:|||||

RESULT 11
ABX99183
ID ABX99183 standard; DNA; 2520 BP.
XX
AC ABX99183;
XX
XX
XX 20-MAY-2003 (first entry)
XX
XX
DE C. peltaci genomic DNA sequence CP4 #4 #2.
XX
XX
XX DNA vaccine; chlamydia infection; blindness; mastitis; infertility;
XX abortion; sexually transmitted disease; atherosclerotic plaque; ds;
XX community-acquired pneumonia; coronary heart disease.
XX
XX Chlamydia peltaci.
XX
XX US2002183272-A1.
XX
XX
XX 05-DEC-2002.
XX
XX 17-DEC-2001; 2001US-0023437.
XX
XX 16-AUG-2000; 2000US-225839P.
XX
XX (JOHN/) JOHNSTON S A.
XX (STEM/) STEWKE-HALE K.
XX (SYKE/) SYKES K F.
XX (KALT/) KALTENBOECK B.
XX
XX Johnston SA, Stewke-Hale K, Sykes KF, Kaltenboeck B;
XX
XX WPI, 2003-328634/31.
XX P-PSDB; ABU66267.
XX
XX
XX New vaccine comprising a polynucleotide with a Chlamydia sequence or a
XX Chlamydia antigen, for inducing an immune response against Chlamydia
XX peltaci, Chlamydia pneumoniae, other Chlamydia species, or a
XX non-chlamydia infection -
XX
XX
XX Claim 6; Page 46-47; 100pp; English.
XX
XX
XX The invention relates to a vaccine comprising a pharmaceutical carrier
XX and at least one polynucleotide having a Chlamydia sequence or at least
XX one Chlamydia antigen. The polynucleotide sequences are obtained
XX from cloned expression library of fragmented genomic DNA (expressed in
XX the vector pCMV-Ub1(+P3). Also included are immunizing an animal
XX comprising providing to the animal at least one Chlamydia antigen or its
XX antigenic fragment (expressed from the cloned polynucleotides) to induce
XX an immune response (the proteins are chosen by transforming a vertebrate
XX animal with constituents of the library and choosing those which elicit
XX the best immune response, and then expressing those clones in cell

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CC culture and purifying the protein), preparing antibodies against a
 CC Chlamydia antigen (comprising identifying a Chlamydia antigen that
 CC confers immune resistance against chlamydia bacterial infection when
 CC challenged with the Chlamydia species in which the antigen was prepared,
 CC generating an immune response in a vertebrate animal with the identified
 CC antigen, and obtaining antibodies produced in the animal, the antibodies
 CC are used to assay for the presence of chlamydia infection in a vertebrate
 CC animal) and testing for antigens for a first disease state/infectious
 CC agent (comprising determining an antigenic polypeptide or a nucleic acid
 CC encoding an antigenic polypeptide from a second disease state or
 CC infectious agent, obtaining a homologue of the antigenic polypeptide or
 CC a nucleic acid encoding an antigenic polypeptide from a second disease
 CC state or infectious agent for the first disease state/infectious
 CC agent, and testing the homology to see if it is an antigenic
 CC polypeptide or a nucleic acid encoding an antigenic polypeptide for the
 CC first disease state or infectious agent). The vaccine, antigens and
 CC polynucleotides are useful for inducing a protective immune response in
 CC vertebrate animals against C. psittaci, C. pneumoniae, other species of
 CC Chlamydia, or a non-chlamydia infection. The antigens are also useful for
 CC antibody preparation techniques. Chlamydia species are also useful for
 CC for blindness, sexually transmitted disease, community-acquired
 CC pneumonia and act as co-factors in atherosclerotic plaque formation in
 CC coronary heart disease. C. psittaci in particular is a cause of mastitis,
 CC infertility and abortion in cattle. The present sequence is one of the
 CC cloned Chlamydia psittaci genomic DNA fragments of the invention.

XX Sequence 2520 BP; 774 A; 584 C; 490 G; 672 T; 0 other;

Alignment Scores:

Pred. No.:	1.39e-103	Length:	2520
Score:	1497.00	Matches:	1357
Percent Similarity:	56.21%	Conservative:	132
Best Local Similarity:	41.03%	Mismatches:	321
Query Match:	34.85%	Indels:	60
DB:	25	Gaps:	25

US-09-830-446-27 (1-841) x ABX99183 (1-2520)

QY 1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
 DB 1 ATGAACATCACTGATCTGTTTAAATTC-----TCGAGCCTATTGGCTCGAAT 54
 QY 21 LeuLeuGlyAlaAlaThrThrGluGlu-----LeuSerAlaSerAsnSerPheAspGly 38
 DB 55 TCTTTGAGCTCCGTAACGACGCTCAACAGCCTTAACCTCCGATCGATCTAATAGA 114
 QY 39 ThrThrSerThrThrSerPheSerSerLeuThrSerSerAlaThrAspGlyThrAsnTyr 58
 DB 115 AATGTGACCTCTGAGAGGTTCCAGGTAAAGAACTTCATCA-----GGAAACAACGTAT 168
 QY 59 ValPheLysAspSerValValIleGluAsnValProLysThrGlyGluThrGlnSerThr 78
 DB 169 ACTGTGAGAGCAATGTGTATCTCTTTCAGGGGAAAGATTTCAGGCTTAAAGAAA--- 225
 QY 79 SerCybPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyPheSer 98
 DB 226 AGTTGTTTC-----TCAGCTACGATTAACCTTACCTTCAGGAAAGGGTATACT 276
 QY 99 PheThrPheSerSerIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAla 118
 DB 277 CTTCCTTGTATATATATTACTACTACGCTAAGTAAACCCCGAGCATTAATGTTCAGGT 336
 QY 119 AlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAla 138
 DB 337 CAAGGAAAAACCTTAGCATCTCAGATTTCTTATTTTCAATGTCTTATTCCTCCA 396
 QY 139 SerThrValThrAsnGlyLeuGlyAlaIleAsnValIleGlyAsnLeuSerLeuAsp 158
 DB 397 GGC-----ACAACGTGGTACGAGCTATACAGACTAAGCAACAACACTTTAAAGAT 450
 QY 159 AsnAspLysValLeuIleGlnAspAsnPheSerThrGlyAspGlyValAlaIleAsnCys 178
 DB 451 AACCTAGTCTGTCTTCATTAATAAACTGCTCAACAGACAGAGGTGGGCTATTCAGTGT 510

QY 179 AlaGlySer-----LeuLysIleAlaAsnAsnLysSerLeuSerPheIleGly 194
 DB 511 AAGAGAAAGCAAGTATGCTGAATTTAAABATTAABAAATATACAGAAATCTGTTTCTCAGA 570
 QY 195 AsnSerSerSerThrArgGlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGly 214
 DB 571 AACCTCTCCACTCAAAAGCGGGGCTATTATTAATGATTAATCACTCAACATTTGCTCAGGT 630
 QY 215 GlyGluThrLysPheGlnGlyAsnThrAlaProThrAlaAlaGly---LysGlyGlyAla 233
 DB 631 GGGCTCACTATTATTTCTAACCACTCTGATTCACAGGTTCAATCCCTTAAGCGGAGCT 690
 QY 234 IleAlaIleAlaAsp---SerGlyThrLeuSerIleSerGlyAspIleIle 252
 DB 691 ATTAGCATTAATAAATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 750
 QY 253 PheGlyGlyAsn-----ThrIleGlyAlaThrGlyThrValSerHisSerAla 268
 DB 751 TTCGATGGGAAACAAATCATCAAACTAGTGTGAAAGTTCTCAAGTAAACAAAGAAATTC 810
 QY 269 IleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyHisThrIle 288
 DB 811 ATGATCTCTGGCACA---GGGAAATTTACAAAGCTACGTCTAAAGACGCTTCGGAAT 867
 QY 289 TyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsnIle 308
 DB 868 TTCCTTATGACCTTATTAACCTGAGGAGATCT-----GATGACCTTAACATT 915
 QY 309 AsnSerProAspThrGlyAspAsnLysGlyTyrThrGlyThrIleValPheSerGlyGlu 328
 DB 916 AATTAATAAAAGAACTGTGAT-----TATACAGAAAGATCGCTCTTCAGGTGA 966
 QY 329 LysLeuThrGluAlaGluAlaLysAspGlyLysAspArgThrSerLysLeuLeuGlnAsn 348
 DB 967 AATTTATCCGATTAAGAAAAGCAAGCAGGAAACCTAGCTTCACTTCAACCAACC 1026
 QY 349 ValAlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAlaAsnGly 368
 DB 1027 ATCACTATTATACAGAGATCTCTGATCTTAAGATGATGATGATGATGATGATGATGATGAT 1086
 QY 369 PheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeu----- 385
 DB 1087 GTAACCGAGAAAGCGGATCTACCTGATCATGATGATGATGATGATGATGATGATGATGAT 1146
 QY 386 ValAlaAsnThrGlnSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArg 405
 DB 1147 TCTTCAGGTGAGAAACATACACCTTAATCTGATTAATTAACATCGCTGTTGGGG 1206
 QY 406 AsnGly-----LysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArg 422
 DB 1207 GGGGGGGGGGATCTCTCTGCTTAATCTGCAACAAATTAACAGCTCAAGCTATTAAT 1266
 QY 423 IleAspArgProValValLeuAlaIleSerAspGlySerPheTyrGlnAsnGlyPheLeu 442
 DB 1267 ATTAAC---GCTGTCAATCTAGTCGATGATGATGATGATGATGATGATGATGATGATGAT 1323
 QY 443 AsnGluAspHisSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleValIle 462
 DB 1324 GCTACGCTTAACCTTTCACAGCAATAGTACCACTAAGCCTAGTACAGTACACAG 1383
 QY 463 SerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGlyLysTyr 482
 DB 1384 CTTACAGATTAATTAACAAATTAATGCTCTCTCACTCACTTACGTTTCCAGGAAATG 1443
 QY 483 ThrIleAsnTyrSerThrAsp-----AspLysLysAlaThrValSerTyrAlaLysGln 500
 DB 1444 ACAAGTAATTTGGGACACCGAAACAGCTACAAAGAACAGCACTTAATTTGGGAAACAACT 1503
 QY 501 SerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTyrGlySer 520
 DB 1504 GGCTACTCCCTTAACCAAGACGTCMAAGACCTTAATGATCCCAATTAATCTTTGGGGGTGCA 1563

QY	521	PhelleAepValAgsSerPheGlnAAspHehIleGluLeuGlyThrGluValAProTyr	540
Db	1564	TTCTCTAAGCTCTCAAGCTATCAAAACTTAATGGATATTAGCGTCATAGCGCTGACTAC	1623
QY	541	GluLysaRphetTPValAlaGlyIleSerAnValLeuNiIaRgsSerGlyArgGluAsn	560
Db	1624	CATAGAGGATTTTGGGTATCCGGTCTAGCTAACTTTCACAAAAGTGGCTGGTAACT	1683
QY	561	GlnArgLysPheAaGhIleValSerGlyValAlaValAlaGlyAlaSerThrArgMetPro	580
Db	1684	AAAGGCAAGTTCGGTCACATATAGGCGCGGATACGGTTTAGCGGTACGCAAAAATCTCT	1743
QY	581	GlyLysPheRThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgPheLysAspTyrPhe	600
Db	1744	TCGTATGATATATTTCAAGTGGCGCTTTCTGGCAACTCTTCGGAAAAGCAAGACTATTTA	1803
QY	601	MetAnthrAenPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnIleAspAlaSer	620
Db	1804	GTGGTCGAAAAACAACGCGCAATTTACGCAAGTTCTCTATATACAGCAT--ATCTCC	1860
QY	621	LeuLysSerValSerIleLeuLeuGlyGluGlyLysLeuArgGluIleLeuLeuPro	640
Db	1861	TATTGAGC-----GTTGGCAAGATCTGCTCAAAAAC	1893
QY	641	TyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyNiIaRAsp	660
Db	1894	ACTATCGGTGCAAGACGTCGGTATGCTCTTAACGACAGATTACTATTATGCAAGCTTCA	1953
QY	661	HisArgMetLysThrGlu-----SerLeuProProProProThrLeuSerThr	677
Db	1954	AACGACATGAAAAACCAACATGACAGCTATACGCTCTCTGTAACCAACGTAAGCAAA	2013
QY	678	AspHisThrSerTPGlyGlyTyrValIlePheAlaGlyLysLeuGlyThrArgValAlaVal	697
Db	2014	ATCAAGGCTGATTTGGGGTAAAGATTTGTTCCGAGTCAGACTGGGCAACTGCTGCTATC	2073
QY	698	GluAsnThrSerGlyArgGlyPhePheGlnGluTyrThrProPheValIleValAlaIle	717
Db	2074	CAACAGAACTCTCTCCTC---CTATTGATATGTATCTACACCTTTCCTGAATTTCAACT	2130
QY	718	ValTyrIleArgGlnAspSerPheValGluLeuGlyAla--IleSerArgAspPheSer	736
Db	2131	GTGCATACGACCAAGATGACTTTTAAAGAAAAACATATGACATCAGGGAAGTACTTCCAA	2190
QY	737	AspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLysLeuGluLysArgPheAla	756
Db	2191	AGCGCAATCTCAACCAACCTTCTCTGCTATCGGCATCACTAAAGTTTGAAG--AGATTGCT	2247
QY	757	GluGln-----TyrTyrHisValAlaAlaMetTyrSerProAspValCysArgSer	773
Db	2248	AACAACGATACAGCTTCTTATCATGATCACTGCTGCTATTTCCTCGATATATGTAAGAGT	2307
QY	774	AsnProLysCysThrThrThrLeuLeuSerAsnGlnLysSer-----TyrLysThrLys	791
Db	2308	AAACCTGACTGTACACTCTCTGTATATTAAGACCCCGCACTGCTGCTGGGTAAACAAA	2367
QY	792	GlySerAsnLeuAlaArgGlnAlaGlyIleValAlaSerGlyPheArgSerLeuGly	811
Db	2368	GCCAAACACTTGGCGCGAAGGCCCTTCATGCTCAACAGCAAGAAATCTACTTGTCTTAAGT	2422
QY	812	AlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTyrPargGlySerSerArgSerTyr	831
Db	2428	CACAACATATGAATCTTCAGCGCAAGTTCCGGTTTCAGACTCAGGGGATCTTCACGAACCTAT	2487
QY	832	AsnValAspAlaGlySerTyrIleLysPhe	841
Db	2488	AACGTAGATCTCGAATCGAAGATTCAGATTC	2517

RESULT 12
ABL91241
ID ABL91241 standard; DNA; 2787 BP
XX
AC ABL91241;

DT	29-JUL-2002	(first entry)
XX		
DE	Chlamydia pneumoniae cp6733 ORF DNA, SEQ ID NO:116.	
XX		
KW	Chlamydial infection; antigen; immunogen; vaccine; diagnosis;	
KW	human respiratory disease; cardiovascular disease; atherosclerosis;	
KM	coronary artery disease; carotid artery stenosis; myocardial infarction;	
KM	cerebrovascular disease; aortic aneurysm; claudication; stroke;	
KM	strain CML029; open reading frame; ORF; gene; ds.	
OS	Chlamydia pneumoniae.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	1..2787
FT		/tag= a
FT	sig_peptide	/product= "cp6733"
FT		1..51
FT		/tag= b
FT	mat_peptide	52..2784
FT		/tag= c
FT		/product= "mature protein"
XX		
PD	MO200202606-A2.	
XX		
PN	10-JAN-2002.	
XX		
PP	03-JUL-2001; 2001MO-IB01445.	
XX		
PR	03-JUL-2000; 2000GB-0016363.	
PR	11-JUL-2000; 2000GB-0017047.	
PR	21-JUL-2000; 2000GB-0017983.	
PR	07-AUG-2000; 2000GB-0019368.	
PR	18-AUG-2000; 2000GB-0020440.	
PR	14-SEP-2000; 2000GB-0022583.	
PR	10-NOV-2000; 2000GB-0027549.	
PR	22-DEC-2000; 2000GB-0031706.	
XX		
PA	(CHIR-) CHIRON SPA.	
PI	Rattl G, Grandt G;	
XX		
DR	WPI; 2002-154726/20.	
XX	N-PDB; ABB90583.	
PT		
PT	Novel Chlamydia pneumoniae protein useful in the manufacture of a	
PT	medicament for treatment or prevention of infection due to Chlamydia,	
PT	preferably Chlamydia pneumoniae, and for diagnostic purposes -	
XX		
PS	Claim 5; Page 97; 364pp; English.	
XX		
CC	Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia	
CC	pneumoniae (strain CML029), and ABL91184-ABL91373 represent DNA encoding	
CC	them. The proteins are predicted to be immunogenic and may therefore be	
CC	useful in vaccine production and for diagnostic purposes. Chlamydia	
CC	pneumoniae is a common cause of respiratory disease in humans, and is	
CC	also involved in the development of cardiovascular diseases such as	
CC	atherosclerosis, coronary artery disease, carotid artery stenosis,	
CC	myocardial infarction, cerebrovascular disease, aortic aneurysm,	
CC	claudication and stroke. The proteins and nucleic acids of the invention	
CC	may be used in vaccines and pharmaceutical compositions for the	
CC	prevention or treatment of chlamydial infections, particularly Chlamydia	
CC	pneumoniae infections. The proteins may also be used in the detection of	
CC	Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched	
CC	DNA probe assay or blotting techniques for determining Chlamydia	
CC	pneumoniae gene expression. The present sequence represents a	
CC	specifically claimed DNA which encodes a Chlamydia pneumoniae protein of	
CC	the invention.	
XX		
SD	Sequence 2787 BP; 803 A; 644 C; 574 G; 766 T; 0 other;	
XX		
XX		

Pred. No.: 6.54e-99

Length: 2787

SQ Sequence 2787 BP; 803 A; 644 C; 574 G; 786 T; 0 other
 Alignment Scores: 6.54e-99 Length: 2787
 Pred. No.:

Score: 1435.50 Matches: 340
Percent Similarity: 51.43% Conservative: 147
Best Local Similarity: 35.90% Mismatches: 335
Query Match: 33.42% Indels: 125
DB: 24 Gaps: 15

US-09-830-446-27 (1-841) x ABJ91241 (1-2787)

QY 1 MetIyelleProleuArgPheleuLeuIleSerleuValProthrleuSerMetSerAsn 20
DB 1 ATGAAGACTTCGATCTCTGGGTTTATGTTCTCCGCTTACCTTCTCA---TGTCAC 57
QY 21 LeuLeuGlyValAlaIleThrIleGluGluLeuSerIleSerAsnSerPheAspGlyThrThr 40
DB 58 CTACAGTCACTACTACAGAGAACTTTATCACTGATGATAGCTTATATGAAATATC 117
QY 41 SerThrThrSerPheSerSerIleThrSerSerIleThrAspGlyThrAsnIleValPhe 60
DB 118 GATTCAGAAAGCTTACTCCMAAAACTTCAGCC-----ACACATATATCTCTA 165
QY 61 LysAspSerValIleGluAsnValProIleThrGlyIleThrGlnSerThrSerCys 80
DB 166 ACAGAGAGATGCTCTTTACGAG---CTGGAAAAGGCACTCCCTTATGACAGTTGT 222
QY 81 PheLysAsnAspAlaAlaIleGlyAspLeuAsnPheLeuGlyGlyIlePheSerPheThr 100
DB 223 TTTAAAGCA-----ACACGAGCAAACTTACCTCTTGGGGAAGGTCACTACCTTAAC 276
QY 101 PheSerAsnIleAspAlaThrThrAlaSerGlyValAlaIleGlySerGluAlaIleAsn 120
DB 277 TTTGGCTTTATATGATGCTGACACTCAAGCAGGCTGCT---GCATCTACACAGCAAA 333
QY 121 LysThrValIleThrleuSerGlyPheSerAlaLeuSerPheLeuIleSerProIleSerThr 140
DB 334 AAGAACTTACCTCTCAGGGTTTCTTACTAGATTATATCTCTCTACACAGC 393
QY 141 ValIleAsnGlyLeuGlyValAlaIleAsnValIleGlyAsnLeuSerLeuLeuAspAsnAsp 160
DB 394 GTTACTACAGGTCAAGGAGCGTTTCTCTCAGCAGAGCGCTTAATTTAGAAATATTCGT 453
QY 161 LysValleuIleGluAsnAsnPheSerThrGlyAspGlyValAlaIleAsnValIleGly 180
DB 454 AAACCTGTAGTCTCGGAATTTTCTACGACAGATGTGAGCTATCAAAAGAGCGCTC 513
QY 180 ----- 180
DB 514 TTCCTTTAACTGCGACTCTGAGATGCTCTTTTAAATAACAATCTTCATCAACAAG 573
QY 180 ----- 180
DB 574 GAGAGCAATTCCTACTACAGAGCGGCTCGCATAGCAATAACACAGTTATGTTAGA 633
QY 180 ----- 180
DB 634 TTCCTATTAACATAGCGTCTACGTCAGAGCGCTATGATGATGAAGCAGCTGATA 693
QY 180 ----- 180
DB 694 CTATCGAACAACAATTTCTATATTGGAAGGATGACGCAAACTACTGCGCGTGC 753
QY 181 ----- 181
DB 754 ATCTGCAACACAAAGGAGGATCTCTCGAACTGATTAATCTCTAACATTAAGACTCTG 813
QY 191 SerPheIleGlyAsnSerSerThrArgGlyValAlaIleIleThrIleAsnLeuThr 210
DB 814 ATCTTGCTTCAAACTGACGAAACAAAGCGTGGCCCATTCATGCTAAAAAAGCTAGCC 873
QY 211 LeuSerSerGlyGlyIleThrLeuPheGlnGlyAsnThrAlaProthrAlaAlaGlyLys 230
DB 874 CTATTCCTGAGGCTTACAGAGTTCTACGAAATATATGCTCATAGCAACTCTCTAG 933
QY 231 GlyGlyAlaIleAlaIleAlaAspSerGlyThrleuSerIleSerGlyAspSerGlyAsp 250

DB 934 GGGGGTGTATCAGCATCATGCTCAGAGAGCTCAGTCTTCTGACAGACAGAAAC 993
QY 251 IleIlePheGluGlyAsnThrIle-----GlyAlaThrGlyThrValSerIleSer 267
DB 994 ATTACCTTTGTAAAGAAATACCTTACACACACCGGAAGTACGATCTCTAAACGTAA 1053
QY 268 AlaIleAspLeuGlyThrSerAlaIleIleThrAlaLeuAspAlaIleGlnGlyIleThr 287
DB 1054 GCATTAACATAGAGATGAAACCGGAATTCACGGAATTCAGGCTCTAAATCATACA 1113
QY 288 IleThrPheThrAspProIleThrValIleThrGlySerThrSerValAlaAspAlaLeuAsn 307
DB 1114 ATTCTCTATATATCCCATCACTTACAGAGAACTCATCA-----CAGCATATGAAG 1167
QY 308 IleAsnSerProAspThrGlyAspAsnIleGlyIleThrGlyIleThrIleValPheSerGly 327
DB 1168 ATAAATTAACGGCTCTGCGGAGCTCAATCCATATCAAGAAAGCATTTCTATTTCTGGA 1227
QY 328 GluLysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSerIleLeuGln 347
DB 1228 GAACCTTACACAGACATGAACTTAAGTTGCTGACAAATTAATCTTCATTCACGCG 1287
QY 348 AsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAlaAsn 367
DB 1288 CCACTCTCCCTATCCGAGAGAAAGTTATGCTACAAAGAGGATCACTTAAGACACAG 1347
QY 368 GlyPheSerGluAspAlaAsnSerIleLeuIleMetAspLeuGlyThrSerLeuValAla 387
DB 1348 AGCTTCTCAAGAGCCGCTTCTCTCCGCGATGATTCAGAGAACATTAATCACT 1407
QY 388 AsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArgAsnGly 407
DB 1408 ACAGCTGGAGATTTCAATACAGACCTTAGCAATCAAGTTACTCTTAGGCTTAAAG 1467
QY 408 LysLysIleLysLeuSerAlaIleAlaThrAlaGlnLysAspIleArgIleAspArgProVal 427
DB 1468 CAGCCGTCAGCTTACACCAAAAGGTCCTCAATTAAGATGCTATCTGGAAGCTC 1527
QY 428 ValLeuAlaIleSerAspGlySerPheIleGlnAsnGlyPheLeuAsnGluAspIleSer 447
DB 1528 AACCTGATTAATGAATGAAGGAACATTTATGAAGCATATGCTTCCAGATGACCGCTC 1587
QY 448 TyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleValIleSerAlaAspSerArg 467
DB 1588 TTC---TCTCTATTAATAATACCGGTTGATGCTGATGTTGATTAACGTTGACATCAGC 1644
QY 468 SerIleAspAlaVal-----GlnSerProIleGlyIleGlnGlyIleGlyIle 482
DB 1645 AGCTTATCCCTGTTCTCTGCTGAGATCTTAATTCGAATTAAGGATTCACAGACATAG 1704
QY 483 ThrIleAsnThrSerThrAsp-----AspLysLeuAlaThrValSerThrAla 498
DB 1705 AATGTTAATTTGACCTACGATACAGTACCAATATACAAAGAGCGCCAGCAACTTGAGCC 1764
QY 499 LysGlnSerPheAsnProthrAlaGluGlnGluAlaProIleValProAsnLeuLeuTrp 518
DB 1765 AAAACAGATTTGTTCCAGCCCGGAAGAAATAATGCGGTGATATAGCAATACCTTAGG 1824
QY 519 GlySerPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAla 538
DB 1825 GAGGCTTACTAGACATTCGCTCTCGCAACAGCTTGAGAGATCGCGCGAATCGGTATAG 1884
QY 539 ProIleGluLysArgPheThrValAlaGlyIleSerAsnValLeuIleAspSerGlyIleArg 558
DB 1885 GAACACAAACAAAGTTTCTGGGTTTCTCCATGACCAACCTCTCTGATATAGACTGAGAT 1944
QY 559 GluAsnGluArgLysPheArgIleValSerGlyValAlaValAlaGlyLysSerThrArg 578
DB 1945 GAATATCGCAAGGCTTCCGTCATACCTCTGAGAGCTACGTCATCGGTGAAGTCTCAC 2004
QY 579 MetProGlyLysPheThrleuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAsp 598

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Db      2005 ACTCCATAAGACGACCTATTACCTTGGCGTTCGACATCTCTTGTTCAGACAAAGAT 2064
QY      599 TyrPheMetAenThrAsnPheAlaIyThrTyrAlaGlySerLeuArgLeuGlnHisAap 618
Db      2065 TGTTTATCGCTCACACAACTTACAACTAGACGGTAACTTATTTCTTCAAGCACTCT 2124
QY      619 AlaSerLeuTyrSerValValSerIleLeuLeuGlyGlyGlyLeuArgIleLeu 638
Db      2125 CATACCTTACAAACCCAAACATATTGAGATTAGAGAAAGCAAAATTTTCTGAACAGCT 2184
QY      639 LeuProTyrValSerIyThrLeuProCysSerPheTyrGlyGlyLeuSerTyrGlyHis 658
Db      2185 ATAGAAAAATTCCTCCAGGAAATTCCTCCAGCTTCGATGATCCAAATTCCTGTCAGCCAT 2244
QY      659 ThrAspHisArgMetLeuThrGlu-----SerLeuProProProProProThrLeuSer 676
Db      2245 TCAGACAAACCGATAGAAACGACATACCTCATTCGCA----- 2283
QY      677 ThrAspHisIleThrSerTyrGlyGlyTyrValTyrAlaGlyLeuGlyThrArgValAla 696
Db      2284 GAATCCGAAGTTCCTTGGAGCAACAGTGTATAGCTGGTGGATAGCGCTACAGCTTCTCT 2343
QY      697 ValGluAenThrSerGlyArgGlyPhePheGlnGlyTyrThrProPheValIyValGln 716
Db      2344 TTGTGTCCTTCCAACTCCATCTCTTCCAAAGCTTCATTCACAGATGAAAGTCGAA 2403
QY      717 AlaValTyrAlaIyArgIleAspSerPheValGlyLeuGlyAlaIleSerArgAspSer 736
Db      2404 ATGTGTTATGATACAAATAATAGCTTTCGAAAGCTTATGATAGCGCTGCTTATAGT 2463
QY      737 AspSerHisIleTyrAsnLeuAlaIleProLeuGlyIleIy-----LeuGlyIyAspPhe 755
Db      2464 ATTTGAGAGCTGCTTAACTCTCGATCTCTGGGGCGGCAAAATGCTGCAAGGGGATATC 2523
QY      756 AlaGlnGlnTyr--TyrHisValValAlaMetTyrSerProAspValCysArgSerAsn 774
Db      2524 GGAGATTCCTACACCTATGATCTCTCAGGATCTTCTTCCAGATGTCATGTAACAT 2583
QY      775 ProIyAsCysThrThrThrLeuSerAsnGlnGlySerThrIyThrIyAspIleSerAsn 794
Db      2584 CCCCAATCTACAGCGACTCTTGATAGACCCCAAGACTCTTGAATAATTCGGCGTGCAT 2643
QY      795 LeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAla 814
Db      2644 CTTTCAAGACAGGACTTTTACAGAGGGTATGCAACAACCTACAGCTCAATTCCT 2703
QY      815 GluLeuPheGlyAsnPheGlyPheGlyTyrPargGlySerSerArgSerTyrAsnValAap 834
Db      2704 GAGCTCTTCGACATTAACCTATGAACTCCGTGATCTTCAAGAACTACATATGATAT 2763
QY      835 AlaGlySerLeuIleIyAspPhe 841
Db      2764 GTTGTACCAAACTCCGATTC 2784

RESULT 13
AAA30847
ID      AAA30847 standard; DNA; 2950 BP.
AC      AAA30847;
DT      29-AUG-2000 (first entry)
XX      Chlamydia antigen CPN100634 full length coding sequence.
DB      Chlamydia antigen CPN100634 full length coding sequence.
XX      Chlamydia antigen; diagnosis; infection; community acquired pneumonia;
KW      therapy; upper respiratory tract disease; bronchitis; sinusitis;
KW      asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthma;
KW      de.
XX      Chlamydia pneumoniae.
XX      Key Location/Qualifiers
XX      CDS 101..2887

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FT      /*tag= a
FT      /product= Chlamydia antigen CPN100634
XX      MO200032794-A2.
XX      08-JUN-2000.
PD      01-DEC-1999; 99WO-CA01147.
XX      01-DEC-1998; 98US-0110339.
PR      01-DEC-1998; 98US-0110340.
PR      01-DEC-1998; 98US-0110427.
PR      01-DEC-1998; 98US-0110428.
PR      01-DEC-1998; 98US-0110438.
XX      (CONN-) CONNAUGHT LAB LTD.
XX      Murdin AD, Oomen RP, Wang J;
XX      WPI; 2000-412339/35.
XX      P-PEDB; AAY90236.
DR      Nucleic acids encoding polypeptide antigens from Chlamydia useful for
PT      preventing, diagnosing and treating diseases such as community acquired
PT      pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
PT      asthma -
XX      Claim 2, Fig 1, 17pp; English.
XX      This sequence encodes a Chlamydia antigen of the invention, designated
XX      CPN100634. The nucleic acids (and their complementary sequences) may be
XX      used as diagnostic agents for detecting the presence of nucleic acids
XX      encoding Chlamydia antigens in samples according to standard methods,
XX      and therefore, for diagnosing Chlamydia infections. For example, they may
XX      be used as primers and probes for diagnostic polymerase chain reaction
XX      (PCR) assays. Antisense sequences may be used to down regulate
XX      expression of the proteins and may be used to treat infections. The
XX      nucleic acids may also be used to produce the protein antigens they
XX      encode according to standard recombinant DNA methodologies. The
XX      proteins may then be used as antigens for the production of antibodies
XX      (i.e. as vaccines) for preventing infection by Chlamydia. The
XX      antibodies may also be used as diagnostic reagents for detecting
XX      CC infections. Chlamydia is a pathogen implicated in the development of
XX      (for example) community acquired pneumonia, upper respiratory tract
XX      disease (especially bronchitis and sinusitis, asthmatic bronchitis,
XX      adult-onset asthma and acute exacerbations of asthma in adults.
XX      5Q Sequence 2950 BP; 851 A; 670 C; 596 G; 833 T; 0 other;
XX      Alignment Scores:
XX      Pred. No.: 7,02e-99 Length: 2950
XX      Score: 1435.50 Matches: 340
XX      Percent Similarity: 51.43% Conservative: 147
XX      Best Local Similarity: 35.90% Mismatches: 335
XX      Query Match: 33.42% Indels: 125
XX      DB: 21 Gaps: 15
XX      US-09-830-446-27 (1-841) x AAA30847 (1-2950)
QY      1 MetIyGlyIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
Db      101 ATGAGACTTCGATTCCTGGGTTTATGTTCTCCGTTGATGCTTCTCA---TGTCA 157
QY      21 LeuLeuGlyAlaAlaIleThrThrGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40
Db      158 CTACAGTCACTAGACGAGAACTTTATCACTGATGATAGCTTTATATGAAATATC 217
QY      41 SerThrThrSerPheSerSerIyThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
Db      218 GATTACAGAACTTATCTCCAAAACCTTCAGCC-----ACAACATATTCCTCA 265
QY      61 IyAspSerValIleGluAenValProIyThrGlyIyThrGlnSerThrSerCys 80

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Db 266 ACGAGATGCTCTTTACGAG---CTGGAAAGGCACTCCCTATCTGACAGTGT 322
 Qy 81 PhelysabaapalaalaaaglyAspLeuAsnPhelLeuylglyGlyPheSerPheThr 100
 Db 323 TTTAAGAA-----ACACGAGCAATCTTACCTCTTGGGAAAGGTCTACAGCTTAAG 376
 Qy 101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAsn 120
 Db 377 TTTGGCTTTATGATGCTGACACTCACTGAGGCTGCT---GCATCTACACAGCAAT 423
 Qy 121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuysSerProAlaSerThr 140
 Db 434 AAGAAATCTTACCTCTCAGGGCTTCTCTTACTGAGTTTATTCCTCTCTACACAAAG 493
 Qy 141 ValThrAsnGlyLeuGlyAlaAlaIleAsnValLysGlyAsnLeuSerLeuAspAsnAsp 160
 Db 494 GTTACTACAGGTACGAGAAAGCGCTTCTCTGACGAGAGCGCTAAATTGAAATATTGCT 553
 Qy 161 LysValLeuIleGlnAspAsnPheserThrGlyAspGlyAlaAlaIleAsnCybalagly 180
 Db 554 AAACCTGAGTCTGCGAATTTTCTACTGACAGATGCTGAGCTATCAAGAGGCTCT 613
 Qy 180 ----- 180
 Db 614 TTCCTTTAACTGACACTTCTGAGATGCTCTTTTATGTAACAATCTTCTATCAACAAAG 673
 Qy 180 ----- 180
 Db 674 GAGAGCAATTCCTACTACAGCAGGCGCTCGCATAGCAATTAACACAGGTTATGTTAGA 733
 Qy 180 ----- 180
 Db 734 TTCCTATCTAACATAGCGTCTACAGTCAGAGGCGCTATGATGATGAAGCAGCTGATA 793
 Qy 180 ----- 180
 Db 794 CTATCGAACAACAATTTCTATATTTGAAAGGAAATGACACGAAACTACTGCGCGTGC 853
 Qy 181 -----SerLeuylIleAlaAsnLeuysSerLeu 190
 Db 854 ATCTGCAACACCAAGCGAGTGAATCTCTGAACTGAACTGTAATCTCTAACATTAAGACTCTG 913
 Qy 191 SerPheIleGlyAsnSerSerThrArgGlyAlaAlaIleAsnThrLysAsnLeuThr 210
 Db 914 ATCTTGCTTCAACAGTACGAGAAACAGAGGCGTGGCCATCATGCTAAAGAGCTAGCC 973
 Qy 211 LeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAlaGlyLys 230
 Db 974 CTTCCTCTGAGGCTTACAGAGTTCCTACGAATATGCTCATCAGCACTCCCTAAG 1033
 Qy 231 GlyAlaAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSerGlyAsp 250
 Db 1034 GGGGGGTCTATCAGCATCATGCTCTGAGAGCTCATGCTTCTCTGACAGACAGAAAC 1093
 Qy 251 IleIlePheGlnGlyAsnThrIle-----GlyAlaThrGlyThrValSerIleSer 267
 Db 1094 ATTACCTTGTAGAAATACCTCTTACAAACACGGAAGTACCATCTCTTAAACCTAAT 1153
 Qy 268 AlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyAsnThr 287
 Db 1154 GCATCAACATACGAGAAATTCACGGAATTCAGGCTGCTCTAAATTCATTAAC 1213
 Qy 288 IleTyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsn 307
 Db 1214 ATTTCTTCTATATCCATCACTTCAAGAGAACTCATCA-----GACGATTAAGAG 1267
 Qy 308 IleAsnSerProAspThrGlyAspAsnLysGlyTyrThrGlyThrIleValIlePheSerGly 327
 Db 1268 ATAAATTAACGCTCTGCGAGGCTCTCAATCATATCAAGAGAACTTCTATTTCTGAG 1327
 Qy 328 GlnLysLeuThrGluAlaGlyAlaLysAspGlnLysAsnArgThrSerLysLeuLeuGln 347
 Db 1328 GAACCTCAACAGCAGATGAATTAAGTTCGACAAATTAATAATCTTCACTTCAAGCT 1387

Qy 348 AsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAlaAsn 367
 Db 1388 CCAAGTCTCCCTATCCGAGAGAAAGTATGTCTACAAAGAGGACTCTTAGAGACAGC 1447
 Qy 368 GlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeuValAla 387
 Db 1448 AGCTTCTCTCAAGAGCCCGTCTCTCCGCGATGATTCAGGAAGCATTAATATCACT 1507
 Qy 388 AsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArgAsnGly 407
 Db 1508 ACAGCTGGAGATTAATCAATCAAGAACTTAGGAATATGATCTCTTAGGCTTTAAG 1567
 Qy 408 LysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAspArgProVal 427
 Db 1568 CAGCCCTGACGCTAACACCAAAAGGTGCTTCAAAATAAAGTATGCTATCTGGAAGCTC 1627
 Qy 428 ValLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeuAsnGluAspHisSer 447
 Db 1628 AACCTGATTGATATTGAAGGAAACATTTATGAAGTCATATGTCAGCATGACCATC 1687
 Qy 448 TyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleValIleSerAlaAspSerArg 467
 Db 1688 TTC---TCTCTATTAATAATCAAGTGTGATGCTGATGTTGATATCACTTGAACATCAC 1744
 Qy 468 SerIleAspAlaVal-----GlnSerProTyrGlyTyrGlnGlyLysTP 482
 Db 1745 AGCTTATCCCTGTTCTCTGCTGAGATCTCTAATTCGAATTCAGATTCGAAGACATAG 1804
 Qy 483 ThrIleAsnTyrSerThrAsp-----AspLysLysAlaThrValSerTyrAla 498
 Db 1805 AATGTTAATTTGACATACGATACAGTACCAAAATACAAAGAGCCAGCCACTTGAGCC 1864
 Qy 499 LysGlnSerPheAsnProThrAlaGlnGlnAlaProLeuValProAsnLeuLeuTyrP 518
 Db 1865 AAAACAGATTTGTTCCAGCCCGAAAGAAATCGCTTGTATGACATACCTATAG 1924
 Qy 519 GlySerPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAla 538
 Db 1925 GAGTCTTACTGACATTCGCTCTCTGCAACAGCTTGTAGAGATCGGCCCACTGATAG 1984
 Qy 539 ProTyrGluLysArgPheThrPylAlaGlyIleSerAsnValLeuHisArgSerGlyArg 558
 Db 1985 GAACACAAACAGGTTTCTGGGTTCTCTGATGACGAATCTTCTGATTAAGCTGAGAT 2044
 Qy 559 GluAsnGlnArgLysPheArgHisValSerGlyAlaValAlaGlyAlaSerThrArg 578
 Db 2045 GAAATCGCAAGGCTTCGTCATACCTCTGAGAGCTACGTACGTGGAAGTGTCTAC 2104
 Qy 579 MetProGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAsp 598
 Db 2105 ACTCTTAAGACGACCTATTTACCTTGGCTTCTGCACTCTCTTGGTGAACAAAGAT 2164
 Qy 599 TyrPheMetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAsp 618
 Db 2165 TGTATTATGCTCAACAACACTTGAACCTTAGGGAACCTTATTTCTTCAAGCACTCT 2224
 Qy 619 AlaSerLeuTyrSerValValSerIleLeuLeuGlyGlyGlyLysLeuArgGluIleLeu 638
 Db 2225 CATACCTTCAACCCCAAAACTATTTGAGATTAGGAAGACAAAGTTTCTGAATCAGCT 2284
 Qy 639 LeuProTyrValSerLysThrLeuProCysSerPheTyrGlyLysLeuSerTyrGlyHis 658
 Db 2285 ATAGAAAAATTCCTTAGGAAATTCCTCTAGGCTTGGATGTCAGAGTTCTGTTACCAT 2344
 Qy 659 ThrAspHisArgMetLysThrGlu-----SerLeuProProProProThrLeuSer 676
 Db 2345 TCAGACAAACGATAGGAAGCAGATACCTCATTTGCCA----- 2383
 Qy 677 ThrAspHisThrSerTyrGlyLysTyrValTyrAlaGlyGluLeuGlyThrArgValAla 696
 Db 2384 GAATCGAAGTTCCTTGGAGCAACAGATGATAGCTGATGCTGATGCTGAGCTTCTCT 2443

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QY 697 ValGluAenThrSerGlyArgGlyPhePheGluGlyThrProPheValValGln 716
XX ::::: ||||| ::::: ||||| ::::: |||||
DB 2444 TTGTTCTTCCACACCATCTCTTTTCAAGACCTTCACAGATGAATGCA 2503
QY 717 AlaValIYrAlaArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSer 736
XX ::::: ||||| ::::: ||||| ::::: |||||
DB 2504 ATGGTTTATGATACCAAAATAGCTTCTTCGAAACCTCAGAGATGAGCGGTTTATG 2563
QY 727 AspSerIleLeuTyAsnLeuAlaIleProLeuGlyIleLeu---LeuGlnLysArgPhe 755
XX ::::: ||||| ::::: ||||| ::::: |||||
DB 2564 ATTGAAGAGCTCTTAACCTCTCGATCTCTGAGGCGCAAAATTCGTGAGGGGATATC 2623
QY 756 AlaGluGlnTY---TyriIleValAlaIleMetTySerProAspValCysArgSerAsn 774
XX ::::: ||||| ::::: ||||| ::::: |||||
DB 2624 CGAATCTTCAACCTATGATCTCAGAGATCTTTGTTCCGAGTCTATCTGATACAT 2683
QY 775 ProLysCysThrThrThleuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsn 794
XX ::::: ||||| ::::: ||||| ::::: |||||
DB 2684 CCCCAATCTACAGCGACTCTGTGTAGAGCCGACACTCTTGAAAAATTCGCGGTGCAAT 2743
QY 795 LeuAlaATGAlaIleGlyIleValGlnAlaIleSerGlyPheArgSerLeuGlyAlaAlaIle 814
XX ::::: ||||| ::::: ||||| ::::: |||||
DB 2744 CTTCAAGACAGCGACTTTTACTGAGGGGTAGCAACAACCTACACTCCCAATGT 2803
QY 815 GluLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArgSerTyAsnValAsp 834
DB 2804 GAGCTCTTCCGACATTAAGCTATGAACTCCGTGATCTTCAAGAACTACATATGAT 2863
QY 835 AlaGlySerLysIleLeuPhe 841
DB 2864 GTTGGTACCAACTCCGATTC 2884

RESULT 14
AAK06816
ID AAK06816 Standard; DNA; 3200 BP.
XX
AC AAK06816;
XX
DT 26-APR-1999 (first entry)
XX
DE Chlamydia pneumoniae surface exposed protein Omp4 DNA.
XX
KM Omp4; outer membrane protein 4; surface exposed protein; antigen;
XX infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
XX
OS Chlamydia pneumoniae.
XX
XX
FH Key Location/Qualifiers
FH CDS 205..2991
FH FT /*tag= a
XX
PN W09858953-A2.
XX
PD 30-DEC-1998.
XX
PF 19-JUN-1998; 98WO-DK00266.
XX
PR 23-JUN-1997; 97DK-0000744.
XX
PA (BIRK/) BIRKELUND S.
XX (CHRI/) CHRISTIANSEN G.
XX
PI Birkelund S, Christiansen G, Knudsen K, Madsen A;
XX Mygind P;
XX
DR WPI: 1999-105610/09.
DR P-PSDB; AAW88417.
XX
XX
XX Species-specific test for identifying mammals infected with
XX Chlamydia pneumoniae - comprises detecting antibodies specific for
XX outer membrane proteins of C. pneumoniae or nucleic acids encoding
XX these proteins
XX

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PS Claim 6; Page 35-40; 115pp; English.
XX
XX This DNA sequence codes for the novel 98.9 kDa surface exposed
CC protein Omp4 (see AAW88417) of the human respiratory pathogen
CC Chlamydia pneumoniae. By generating antibodies against C.
CC pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
CC was obtained which reacted with outer membrane proteins. The
CC antibody was used to identify the genes (see AAK06816-27) encoding
CC Omp4-Omp5 proteins (see AAW88417-28) in an expression library of
CC C. pneumoniae DNA. The genes are situated in 2 gene clusters:
CC Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
CC the other; and encode polypeptides of about 89.6-100.3 kDa and
CC about 56.1 kDa. The invention provides a new species specific test
CC for identifying mammals (including humans) infected with Chlamydia
CC pneumoniae. The test comprises detecting antibodies specific for
CC Omp4-Omp5 or detecting nucleic acid fragments encoding these outer
CC membrane proteins, especially by PCR. The proteins are also used
CC in the diagnosis of C. pneumoniae infection in mammals. The
CC nucleic acids and proteins can also be used in the immunization of
CC mammals, the nucleic acids being particularly useful as DNA
CC vaccines for effecting in vivo expression of antigens. The
CC vaccines may also prevent atherosclerosis and bronchial asthma,
CC which are possibly associated with C. pneumoniae.
XX
XX Sequence 3200 BP; 946 A; 708 C; 623 G; 923 T; 0 other;
SQ
XX
Alignment Scores:
Pred. No.: 7,786-99 Length: 3200
Score: 1435.50 Matches: 340
Percent Simlarity: 51.43% Conservative: 147
Best Local Simlarity: 35.90% Mismatches: 335
Query Match: 33.42% Indels: 125
DB: 20 Gaps: 15

US-09-830-446-27 (1-841) x AAK06816 (1-3200)
QY 1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
DB 205 ATGAAGACTTGATCCCTGCGTTTGGTTTCCCGGTAGCTTCTCA---TGTCAC 261
QY 21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40
DB 262 CTACAGTCACCTAGCTTAACGAGAACTTTATACACTGATGATACCTTTAAAGCAAAATC 321
QY 41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyValPhe 60
DB 322 GATTCAGAGACGTTTACTCCAAAACCTTCAGCC-----ACAACTATTTCTTA 369
QY 61 LysAspSerValIleGluAsnValProLysThrGlyGluThrGlnSerThrSerCys 80
DB 370 ACAGAGATGATCTTCTTTACGAG---CTGAAAGAGCACTCCCTATCTGACAGTTGT 426
QY 81 PheLysAsnAspAlaAlaIleGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThr 100
DB 427 TTTAAGCAA-----ACCACGCAACATCTTACTTGGGAAACGTCATAGCTTAACG 480
QY 101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsn 120
DB 481 TTGGCTTTATAGATGCTGAGCACTCATGACAGGTCTCT---GCATCTACACAGCAAT 537
QY 121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
DB 538 AAGATCTTACCTTCTCAGGTTTCTTCTTACTGAGTTTGAATCCTCTCTAGCAACAG 597
QY 141 ValThrAsnGlyLeuGlyAlaIleAsnValLysLeuGlyAsnLeuSerLeuLeuAspAsp 160
DB 598 GTTACTACAGCTCAGGAGAACCTTCTCCACAGAGAGCGTAATTTAGAAATATTCTGT 657
QY 161 LysValIleuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly 180
DB 658 AAACCTGATGTTGCTGGAAATTTTCTACTGCAATGTGAGCTATCAAGAGCGTCT 717
QY 180 ----- 180

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QY 815 GtLeuphegLyAsnphedLyPheglutTPArgLySerSerArgSerTyAsnValAsp 834
 DB 2908 GAGCTCTTCGACATTAAGCTATGAACTCGTGGATCTTCAAGAACTACATATAGAT 2967
 QY 835 AlAgLySerLyGtLeuPhe 841
 DB 2968 GTTGGTACCAACTCCGATTC 2988
 RESULT 15
 AAC81914/C
 ID AAC81914 standard; DNA, 273254 BP.
 AC AAC81914;
 XX 27-FEB-2001 (first entry)
 DT Chlamydia pneumoniae genome DNA.
 DE Chlamydia pneumoniae genome DNA.
 XX Genome; diagnosis; vaccine; ds.
 XX Chlamydia pneumoniae.
 OS WO200027994-A2.
 XX 18-MAY-2000.
 PD 12-NOV-1999; 99WO-US26923.
 PF 12-NOV-1998; 98US-0108279.
 PR 08-APR-1999; 99US-0128606.
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX Stephens R, Mitchell W, Kalman S, Davis R,
 DR WPI; 2000-376516/32.
 XX Isolated nucleic acid for use in diagnostic and analytical methods
 PT encodes genomic sequence of Chlamydia pneumoniae -
 PS Claim 2; Page 128-320; 320pp; English.
 XX
 CC This invention describes a novel nucleic acid (N1) encoding a Chlamydia
 CC pneumoniae protein (P1), given in the specification. The isolated nucleic
 CC acid is useful for diagnostic and analytical methods, such as,
 CC hybridization-based assays or amplification-based assays. The protein may
 CC be used for diagnostic purposes, for their enzymatic or structural
 CC activity, or as a vaccine. The invention also describes (1) a probe
 CC comprising a hybridizing fragment of N1; (2) an isolated nucleic acid
 CC (N2) that hybridizes under stringent conditions to N1; (3) an expression
 CC cassette comprising N1 under the transcriptional regulation of a
 CC transcriptional initiation region functional in an expression host, and a
 CC transcriptional termination region; (4) a cell comprising an expression
 CC cassette of (3) as part of an extrachromosomal element or integrated into
 CC the genome of a host cell as a result of induction of the expression
 CC cassette into the host cell; and the cellular progeny of the host cell;
 CC (5) a method for producing a P1 comprising growing a cell of (4) where
 CC the protein is expressed and isolating the protein free of other
 CC proteins; (6) a purified polypeptide composition comprising at least 50
 CC weight % of P1; and (7) a monoclonal antibody binding specifically to the
 CC peptide of (6).
 CC
 CC Sequence 273254 BP; 76423 A; 51054 C; 61965 G; 83812 T; 0 other;
 SQ
 Alignment Scores:
 Pred. No.: 2.1e-96 Length: 273254
 Score: 1435.50 Matches: 340
 Percent Similarity: 51.43% Conservative: 147
 Best Local Similarity: 35.90% Mismatches: 335
 Query Match: 33.42% Indels: 125
 DB: 21 Gaps: 15

US-09-830-446-27 (1-841) x AAC81914 (1-273254)
 QY 1 MetLySileProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
 DB 98031 ATGAAGACTTCGATTCCTTGGGTTTAACTTCCCGGTTAGCTTCTCA---TGTCAC 97975
 QY 21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40
 DB 97974 CTACAGTCACAGCTAACAGAACTTTATCACCTGATGATAGCTTAATGAAATATC 97915
 QY 41 SerThrThrSerPheSerSerLyThrSerSerAlaThrAspGlyThrAsnTyValPhe 60
 DB 97914 GATTCAGGAAGCTTTACTCCAAAACCTTCAGCC-----ACAACTATTTCTCTA 97867
 QY 61 LysAspSerValIleGluAsnValProlyThrGlyGluThrGlnSerThrSerCys 80
 DB 97866 ACAGAGATGTCCTTCTTTAGAG---CTGGAAAAGCAGCTCCTATCTGACAGTTGT 97810
 QY 81 PheLyAsnAspAlaAlaIleGlyAspLeuAsnPheLeuGlyGlyPheSerPheThr 100
 DB 97809 TTTAAGCAA-----ACCACGACAACTCTTCTGGGGAACGGTCATAGCTTAACG 97756
 QY 101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAsn 120
 DB 97755 TTTGGCTTTATGATGCTGGCAGCTCATGAGTCTGCT---GCATCTACACAGCAAT 97699
 QY 121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLySerProAlaSerThr 140
 DB 97698 AAGATCTTACTTCTCTAGGGTTTCTTCTACTGAGTTTGAATCTCTCTCAGCAACAG 97639
 QY 141 ValThrAsnGlyLeuGlyAlaIleAsnValIleGlyAsnLeuSerLeuAspAsnAsp 160
 DB 97638 GTTACTACAGGTCAGGAAACCTTCTCCACAGAGAGCGTAATTTGAAAATATTTGCT 97579
 QY 161 LysValLeuIleGluAsnAsnPheSerThrGlyAspGlyGlyAlaIleAsnTyAlaGly 180
 DB 97578 AAACCTTGATGCTGGGAATTTTCTACAGATGTTGAGCTATCAAGAGAGCGTCT 97519
 QY 180 ----- 180
 DB 97518 TTCCTTTAACTGGCAGCTTCGAGATGCTCTTTTACTAACAACCTTCTCATCAACAAG 97459
 QY 180 ----- 180
 DB 97458 GAGAGGCAATTTGCTACTACAGAGCGCTGCATAGCAATAACACAGATTATGTAGA 97399
 QY 180 ----- 180
 DB 97398 TTCCTATCTAACATAGCGTCTACGAGAGCGCTATCGATGAGAAGCAGCTGATA 97339
 QY 180 ----- 180
 DB 97338 CTATCGAACAACAATTTCTATATTTTGAAGGAAATGAGGAAACCTACGCGGTGCG 97279
 QY 181 -----SerLeuLySileAlaAsnAsnLySerLeu 190
 DB 97278 ATTCGACACCAAGCGAGTGATCTCTGAACTGATTAATCTCAACAATAAGACTCTG 97219
 QY 191 SerPheIleGlyAsnSerSerThrArgGlyGlyAlaIleThrThrLyAsnLeuThr 210
 DB 97218 ATCTTTGCTTCAACGTAAGAAACAAGCGGTGGCGCATTCATGCTAAAAGCTAACCC 97159
 QY 211 LeuSerSerGlyGlyGluThrLeuPheGlnLyAsnThrAlaProThrAlaAlaGlyLys 230
 DB 97158 CTTTCCTCTGAGAGCTTTACAGATTTCTAGAAATATATGCTCATACGAACTCCTAAG 97099
 QY 231 GlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSerGlyAsp 250
 DB 97098 GGGGGTGTATACACATCGATGAGCTCAGAGAGCTCACTTTCTGACAGACAGAAAC 97039
 QY 251 IleIlePheGluGlyAsnThrIle-----GlyAlaThrGlyThrValSerHisSer 267
 DB 97038 ATTACCTTTGTAAAGAAATACCTTACAAACAACGGAAGTACCGATCTCTTAAAGTAAAT 96979

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 29, 2004, 10:21:11 ; Search time 4263 Seconds

(without alignments)
4794.761 Million cell updates/sec

Title: US-09-830-446-27
Perfect score: 4295

Sequence: 1 MKIPILRFLISLVPTISMGN.....FEWRGSSRSYNDAGSKTF 841

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+.p2n.model -DEV=xlh
-Q/cgn2.1/USPTO.spool/US09830446/runat.29012004.102102.19215/app.query.fasta.1.1031
-DB=EST -OPMT=fastap -SUFFIX=2n.rst -MINMATCH=0.1 -LOGOFC=0 -LOGOEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blonum62 -TRANS=human40.cdi -I57=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NOR=ext -HEA5IZE=500 -MINLEN=0 -MAXLEN=200000000
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-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gse_hum:*
18: em_gse_hiv:*
19: em_gse_pih:*
20: em_gse_vit:*
21: em_gse_fun:*
22: em_gse_man:*
23: em_gse_mus:*
24: em_gse_pro:*
25: em_gse_rtd:*
26: em_gse_phg:*
27: em_gse_vrl:*
28: gb_gse1:*

29: gb_gse2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	157	3.7	915	29	CNS06GB1
2	155	3.6	624	12	BM276405
3	155	3.6	979	29	CNS06EDM
4	151	3.5	1094	29	CNS076CM
5	151	3.5	2293	11	AK032791
6	150.5	3.5	1022	9	AL543791
7	150.5	3.5	1792	11	AY103948
8	144	3.4	1164	13	BX405896
9	142	3.3	977	29	CNS0678C
10	142	3.3	1159	29	CNS076BD
11	141.5	3.3	1001	13	BQ963411
12	140.5	3.3	634	10	BE583883
13	140	3.3	779	14	CA318878
14	137.5	3.2	788	12	B3368874
15	135.5	3.2	698	14	CD284689
16	135	3.1	738	14	CA357513
17	135	3.1	739	14	CD459142
18	135	3.1	1150	29	CNS0792S
19	134.5	3.1	719	14	CA855416
20	133.5	3.1	849	28	AZ546009
21	133	3.1	755	14	CA486671
22	133	3.1	761	14	CA484808
23	132.5	3.1	739	28	AY079536
24	132	3.1	882	13	BQ723746
25	132	3.1	898	29	CNS04ALV
26	130.5	3.0	644	13	BO838510
27	130	3.0	731	14	CA485466
28	130	3.0	740	14	CA485375
29	130	3.0	833	12	B329437
30	129.5	3.0	905	29	CNS06LFI
31	129.5	3.0	965	29	CNS07DQ3
32	129	3.0	672	14	CD047378
33	128.5	3.0	926	29	CNS06FRK
34	128.5	3.0	1200	14	CD497556
35	128	3.0	938	29	CNS07CG2
36	127.5	3.0	804	13	BUE02542
37	127.5	3.0	816	28	AZ535744
38	127.5	3.0	863	14	CB588445
39	127.5	3.0	2391	28	BH771003
40	127	3.0	695	12	B3388152
41	127	3.0	807	12	B412244
42	127	3.0	877	28	AZ531291
43	126.5	2.9	832	12	BM170146
44	126.5	2.9	1123	12	BM554825
45	126.5	2.9	2589	11	AK047537

ALIGNMENTS

RESULT 1
CNS06GB1
LOCUS
DEFINITION
T3 end of clone AS0AA003C01 of library AS0AA from strain CLIB 533
of Saccharomyces bayanus, genomic survey sequence.
ACCESSION
AL397475
VERSION
AL397475.1 GI:12150179
KEYWORDS
GSS.
SOURCE
Saccharomyces bayanus
ORGANISM
Saccharomyces bayanus
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE
1 (bases 1 to 915)

AUTHORS Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., Boitton-Fukuhara,M., Bon,E., Brothier,P., Casaregola,S., deMontigny,J., Dujon,B., Durrens,P., Leplingle,A., Lorente,B., Malpertuy,A., Neuvéglise,C., Ozler-Kalogeropoulos,O., Potier,S., Saurin,W., Taketa,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Winkler,P. and Weissenbach,J.

TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies

JOURNAL FEMS Lett. 487 (1), 3-12 (2000)

MEDLINE 20584711

REFERENCE 11152876

AUTHORS 2 (bases 1 to 915)

TITLE Bon,E., Neuvéglise,C., Casaregola,S., Artiguenave,F., Winkler,P., Aigle,M. and Durrens,P.

JOURNAL Genomic exploration of the hemiascomycetous yeasts: 5.

MEDLINE 20584715

REFERENCE FEMS Lett. 487 (1), 37-41 (2000)

AUTHORS 3 (bases 1 to 915)

TITLE Genoscope.

JOURNAL Direct Submission

REFERENCE Submitted (07-SEP-2000) Genoscope - Centre National de Séquençage, 2 rue Gaston Crémieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *uvatum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbicola*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES

source

1..915

/organism="Saccharomyces bayanus"

/mol_type="genomic DNA"

/strain="CUB 533"

/variety="uvatum"

/db_xref="taxon:4931"

/clone="AS0A003C01"

/clone_lib="AS0A"

/note="Tend : 73"

<7..>911

/note="similar to Saccharomyces cerevisiae ORF YIL169c [similarity to glucan 1,4-alpha-glucosidase and YAR066w] 2 putative frameshift(s) similar to Saccharomyces cerevisiae ORF YOL155c [similarity to glucan 1,4-alpha-glucosidase Stalp and YAR066w]"

/evidence=not experimental

BASE COUNT 158 a 256 c 199 g 299 t 3 others

ORIGIN

Alignment Scores:

Pred. No.: 1.4e-05 Length: 915

Score: 157.00 Matches: 83

Percent Similarity: 38.64 Conservative: 70

Best Local Similarity: 20.96 Mismatches: 123

Query Match: 3.66 Indels: 120

DB: 29 Gaps: 15

US-09-830-446-27 (1-841) x CNS06GB1 (1-915)

QY 9 LeuileSerIleValProthrIleuSerMetSerAsnLeuLeuGlyAlaIleThrIleGlu 28

DB 4 GTTTAGCCCTTACTCTCAAGAGTCATTGGCGCAACTATAGCAATATGATCTTCACTT 63

QY 29 GluLeuSerAlaSerAsnSerPheAspGlyThrThrSerThrThrSerPhe----- 45

DB 64 TCAAGCAACACCTCGTCGACCGTTGTCATCACTTCACTTCACTTCACTTCACTTCACTT 123

QY 46 SerSerIleThrSerSerAlaThrAspGlyThrAsnIleValPheIleAspSerValVal 65

DB 124 AGTCATCACTTGT 165

QY 66 IleGluAsnValProIleThrGlyGlyThrGlnSerThrSerCysPheIleAsnAspAla 85

DB 166 -----ACTGGGTCAACTTCGCT----- 183

QY 86 AlaIleAspLeuAsnAsnAsnLeuGlyGlyGlyPheSerPheThrPheSerAsnIleAsp 105

DB 184 -----GGTTCTGGCCCTCA-----AGCTTATTA 210

QY 106 AlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsnIleThrValThrIleu 125

DB 211 GGGTCACCTTGT 270

QY 126 SerGlyPheSerAlaLeuSerPheLeuIleSerProIleAsnThrValThrAsnGlyLeu 145

DB 271 TCCGTGTCTCGAC-----TCATTTACTGGGTCAACTTCGTGTGTCT 315

QY 146 GlyAla-----IleAsnValIleGlyAsnLeuSerIleuAsnAsnAspValLeuIle 164

DB 316 GGCCTCTCAAGCTCTTATTACTGAG----- 339

QY 165 GluAsnAsnPheSerThrIleGlyAspGlyGlyAlaIleAsnCysAlaIleSerIleuIle 184

DB 340 -----TCACTCTGTCGGGTTCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 378

QY 185 AlaAsnAsnIleSerIleSerPheIleGlyAsnSerSerThrIleArgIleGlyAlaIle 204

DB 379 -----CATCTGT 429

QY 205 HisThrIleAsnLeuThrIleuSerSerGlyGlyGlyIleuThrIleuPheGlnIleAsnThrAla 224

DB 430 TCCAGTTCAAGCTCTCATCTGT 477

QY 225 ProThrAlaIleGlyIleGlyGlyAlaIleAlaIleAlaIleAspSerGlyThrIleuSerIle 244

DB 478 CCACTGT 537

QY 245 SerGlyAspSerGlyAspIleIlePheGluIleAsnThrIleGlyAlaThrGlyThrVal 264

DB 538 GCTCTCATCTGT 597

QY 265 SerHisSerAlaIleAspLeuGlyThrSerAlaIleIleThrAlaIleuAsnAlaIleAsn 284

DB 598 TCTGTTCAAGCTCTCGGTTCGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 639

QY 285 GlyHisThrIleIleThrPheThrAspProIleThrValThrGlySerThrSerValAlaAsp 304

DB 640 -----CATCTTACTCAACCGATCCGGTCCCTCAAGTACT 675

QY 305 AlaLeuAsnIleAsnSerProAspThrGlyAspAsnIleGlyThrGlyThrIleVal 324

DB 676 ATCACTCTCTCTCATCTTGT 711

QY 325 PheSerGlyGlyIleuThrGluIleAlaIleAspGlyIleuAsnIleThrSerIle 344

DB 712 GCTCTGTGT----- 720

QY 345 LeuLeuGluAsnValAlaPheIleAsnGlyThrValIleuIleu----- 359

DB 721 -----TCCCTTCTTCTTCAAGATGATCTTATCTTATCACTTCACTTCACTTCACTT 771

QY 360 GlyAspValIleuSerAlaAsnGlyPheSerGlnAspAlaAsnSerIleuIleuMet 379

DB 772 GCGCATATCACTTACCGGTGATGTATTGTCTCAAGTGA-----GTTGAATTC 822

QY 380 AspLeuGlyThrSer-----LeuValAlaAsnThrIleuSer 391

DB 823 GCCGTGSGCAAAATTAACCTTCTTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 870

RESULT 2
LOCUS BM276405/c 624 bp mRNA linear EST 20-DEC-2001
DEFINITION PFES00a82f11.Y1 Plasmodium falciparum 3D7 gametocyte cDNA library
Plasmodium falciparum 3D7 cDNA 5' similar to SW:ClB_DICD1 094481
ClB PROTEIN ; mRNA sequence.
ACCESSION BM276405
VERSION BM276405.1 GI:17969762
KEYWORDS EST.
SOURCE Plasmodium falciparum 3D7
ORGANISM Plasmodium falciparum 3D7
REFERENCE 1 (bases 1 to 624)
AUTHORS Tang,K., Cole,R., Chakrabarti,D., Haywood,R., Clifton,S., Pape,D.,
Marr,K., Hillier,L., Martin,J., Wylie,T., Dante,M., Theising,B.,
Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Jentes,R., Ronho,I.,
Tsagarelashvili,R., Belaygorod,U., Franklin,C., Carr,L., Gtow,A.,
Maguire,L., Richey,J., Madkins,J., Kennedy,S., Levinso,D.,
Waterston,R., Wilson,R. and Sibley,D.
TITLE WASHU Plasmodium EST Project
JOURNAL Unpublished
COMMENT Contact: L. David Sibley
WASHU Plasmodium EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
Library was constructed by R. Haywood. DNA sequencing by:
Washington University Genome Sequencing Center for information on
obtaining a clone please contact: L. David Sibley
(sibley@orcim.wustl.edu), Washington University
Seq primer: -40UP from G1bco
High quality sequence stop: 430.
Location/Qualifiers
1..624
/organism="Plasmodium falciparum 3D7"
/mol_type="mRNA"
/db_xref="taxon:36329"
/dev_stage="gametocyte (stage III-V)"
/lab_host="DH10B (GeneHog, Invitrogen, Inc.)"
/clone_lib="Plasmodium falciparum 3D7 gametocyte cDNA
library"
/note="Vector: pBluescript SK plus; Site 1: EcoRI; Site 2:
XhoI. The library was constructed by R Haywood. cDNAs were
synthesized from gametocyte poly(A)+ RNA by oligo d(T)
priming, size-selected and directionally cloned into the
EcoRI (5' end) to XhoI (3' end) sites of the Uni-ZAP XR
lambda vector (Stratagene). The primary library was mass
excised as phagemid using the ExSist1 helper phage
(Stratagene). Clones were mass excised using the ExSist1
helper phage (Stratagene), the phagemids were precipitated
with PEG 8000 and extracted with phenol/chloroform.
Phagemid DNA was electroporated into DH10B cells. Clone
Availability: David Sibley, Washington University."

BASE COUNT 261 a 61 c 158 g 144 t
ORIGIN

Alignment Scores:
Pred. No.: 1,27e-05 Length: 624
Score: 155.00 Matches: 60
Percent Similarity: 45.65% Conservative: 45
Best Local Similarity: 26.09% Mismatches: 97
Query Match: 3.61% Indels: 28
DB: 12 Gaps: 8

US-09-830-446-27 (1-841) x BM276405 (1-624)

QY 17 SerMetSerAsnLeuGlyAlaIaIaThrThrcIuLeuSerAlaSerAsnSerPhe 36
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DB 623 AGCTTCAGGATGATCTTCTTCTACTAGTCTTCTCGATATACCTCTTCTTCTT 564
|||
QY 37 AspGlyThrThrSerThrThrSerPheSerSerThrThrSerSerAlaThrAspGlyThr 56

DB 563 TCAGGTATCACTTCTTCACTGATTCCTCAGGTATTAATCTTCTTCACTAGT----- 513
|||
QY 57 AantYrValPheLysAspSerValIleGluAenValProLysThrGlyLuhThrgin 76
|||
DB 512 -----TCTTCTGATTAAGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 468
|||
QY 77 SerThrSerCyPheLysAspAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 96
|||
DB 467 TCACTTAAT-----AACTCAGGTATTAATCTTCTTCTTCTTCTTCTTCTTCTTCTT 417
|||
QY 97 PheSerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaIleGlySer 116
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DB 416 TTTTCTTACAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 357
|||
QY 117 GluAlaIa 136
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DB 356 ACTAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 309
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QY 137 ProAlaSerThrValThrAsnGly---LeuGlyAlaIleAsnValIleGlyAsnLeuSer 155
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DB 308 ---TCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 252
|||
QY 156 IeuleuAspAsnAspLysValIleuIleGluAspAsnPheSerThrGlyAspGlyAla 175
|||
DB 251 TCAATCAATTTCTTCTGATTT-----ACTTCTTCAACAACCTTCTTCTTCTTCTT 204
|||
QY 176 IleAsnCyAlaGlySerLeuLysIleAlaIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 195
|||
DB 203 ACTTCTTCAATCAATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 144
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QY 196 SerSerSerThrThrGlyValIleIleIleIleIleIleIleIleIleIleIleIleIle 214
|||
DB 143 TCAATTAAGTCTTCTTCTG-----ACAACCTTTTAATTAATTTCTTCTTCTTCTT 96
|||
QY 215 ---GlyLuhThrLeuPheGlnGlyAsnThrAlaProThrAlaIaIaGlyLysGlyAla 233
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DB 95 ACTTCTTCAATCAATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 39
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QY 234 IleAlaIleAlaAspSerGlyThrLeuSer 243
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DB 38 TCTTCAATTAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 9
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RESULT 3
LOCUS CNS06PDW/c 979 bp DNA linear GSS 05-JUL-2001
DEFINITION T7 end of clone AV0A013G05 of library AV0A from strain CBS 379 of
Saccharomyces exiguus, genomic survey sequence.
ACCESSION AL409242
VERSION AL409242.1 GI:12176588
KEYWORDS GSS.
SOURCE Saccharomyces exiguus
ORGANISM Saccharomyces exiguus
REFERENCE 1 (bases 1 to 979)
AUTHORS Soucier,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Bolotin-Fukuhara,M., Bon,E., Broctier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
Malpeteruy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,M., Tekala,F., Toffano-Nicohe,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
MEDLINE 11152876
PUBMED 20584711
REFERENCE 2 (bases 1 to 979)
AUTHORS Bon,E., Neuvéglise,C., Lepingle,A., Wincker,P., Artiguenave,F.,
Gallardin,C. and Casaregola,S.
TITLE Genomic exploration of the hemiascomycetous yeasts: 6.
Saccharomyces exiguus
JOURNAL FEBS Lett. 487 (1), 42-46 (2000)

MEDLINE 20584716
 PUBMED 1152881
 REFERENCE 3 (bases 1 to 979)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 COMMENT This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *uvarum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbicola*, *Candida tropicalis* and *Xerozyma lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES
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 Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="CBS 379"
 /db_xref="taxon:34358"
 /clone="AY00A013G05"
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 /note="end : 77"
 BASE COUNT 226 a 205 c 217 g 331 t
 ORIGIN

Alignment Scores:
 Pred. No.: 2,536-05 Length: 979
 Score: 155.00 Matches: 83
 Percent Similarity: 37.87% Conservative: 45
 Best Local Similarity: 24.56% Mismatches: 138
 Query Match: 3.61% Indels: 72
 DB: 29 Gaps: 13

US-09-830-446-27 (1-841) x CNS06PDM (1-979)

26 ThrThrglgluLeuSerAlaSerAnSerPheAepgLyThrThrSerThrSerPhe 45
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 885 ACAACTGATGATTAATGATGCTCAACTACACAGAACTGGGCAACCGATGTAAT 826
 46 SerSerLyThrSerSer-----AlaThrAepgLyThrAenTyValhels 61
 |||||
 825 GGTCTCAAACTACACAGAACTGGTGAACCTGATGTAATGCT----- 778
 62 AspSerValValIleGlubAnValProLyThrGlyLutThrGlnSerThrSerCySph 81
 777 -----TTCCAAACTACACAGAACTGGT----- 751
 82 LybAenAepAlaAlaGlyAepLeuAnPheLeuGlyGlyPheSerPheThrPhe 101
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 750 GCAACTGAT-----GGTAATGGTTCTCAAACTACCAACC 718
 102 SerAnIleAepAla-----ThrThraLaseGlyAlaAlaIleGlySerGluAla 118
 |||||
 717 GATGTAATAGTGTCTCAAACTACACAGAACTGGTGAACCGATGTAAT----- 664
 119 AlaAenLyThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLySerProAla 138
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 663 ---GGTTCACAACTACACAGAACTGGTGAACCTG-----GGTAATGGTTCT 613
 139 SerThrValThrAenGlyLeuGlyAlaIleAenValLyGlyAenLeuSerLeuLeuA 158
 |||||
 612 CAAACTACACACTACAGAACTGGTGAACCGATGTAATGCTTTTAACCTACCAACTGAT 553
 159 AenAepLyValLeuIleGlnAepAnPheSerThrGlyAepGlyValAlaIleAnCyS 178
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 552 GATTAATAGTCT-----CAAACTACACACTACAGAACTGGTGAACCGATGCT 505
 179 AlaGlySerLeuLyIleAlaAenAnLySerLeuSerPheIleGlyAenSerSer 198

DB 504 AACGCTCTTTA-----ACAAACC 487
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 Cy 199 ThrArgLyGlyAlaIleHisThrLybAnLeuThrLeuSerSerGlyGlyThrLeu 218
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 Db 486 ACTACAGGAAGACTGGTGAACCTGATGTAATGCTCTTTTAACCTACGAATGATTAATAGT 427
 219 PheGlnGlyAenThrAlaProThrAlaAlaGlyLyGlyGlyAlaIleAlaIleAep 238
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 Db 426 GCTCAAAATTACAACTACAGAACTGGTCAACTGATGTAATGTTCTCAAACTACCAACC 367
 239 SerGlyThrLeuSerIleSerGlyAepSerGlyAepIleIlePheGlyAenThrIle 258
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 Db 366 GATGTAATGGTTCTCTACACAACTACAGAACTGGTGAACCGATGTAATGCTTCT 307
 259 GlyAlaThr-----GlyThValSerHisSerAlaIleAepLeuGlyThrSerAlaLyS 276
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 Db 306 CAAGTACAACTGATGTAATGCTTTTAACCTCAACTGAT---GGTAACAGTCTTCA 250
 277 IleThr-----AlaLeuAArgAlaIleGlnGlyHisThrIleTyPheTy 291
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 Db 249 ACTACAACTGATGCAATGCTTCTTAACCTCAACCGATGTAACAGTCT----- 199
 292 AspProIleThrValThrGlySerThrSerValAlaAepAlaLeuAenAnSerPro 311
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 Db 198 ---CAAACTACACACTACAGAACTGGTCAAAATCCGATGCAACAGATGTAACGCTTCC 142
 312 AspThrGlyAepAnLySerGlyThrGlyThrIleValPheSerGlyGlu----- 328
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 Db 141 CAACACAGATGATGTAATGTAATGTAACATACGCAACTAATGCTGATGTAATGAG 82
 329 -----LybLeuThrGluAlaGlyAlaLybAepGlyLybAenAnGThrSer 343
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 Cy 81 ATGGATCATCATCAATGATGCTAATGATGGAACAATCTACAGAAACAAGC 28

RESULT 4
 CNS076CM/
 LOCUS
 DEFINITION T3 end of clone BBOA002P11 of library BBOA from strain CBS 4732
 ACCESSION AL431228
 VERSION AL431228.1 GI:12214640
 KEYWORDS GSS.
 ORGANISM *Pichia angusta*
 SOURCE *Pichia angusta*
 ORGANISM *Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.*
 REFERENCE 1 (bases 1 to 1094)
 Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G., de-Montigny,J., Dujon,B., Durieux,P., Lepingle,A., Lorente,B., Malpertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Wincker,P. and Weissenbach,J.
 Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
 Yeast 19: 487 (1), 3-12 (2000)

TITLE
 JOURNAL MEDLINE 20584711
 PUBMED 1152876
 REFERENCE 2 (bases 1 to 1094)
 Blandin,G., Lorente,B., Malpertuy,A., Wincker,P., Artiguenave,F. and Dujon,B.
 Genomic exploration of the hemiascomycetous yeasts: 13. *Pichia angusta*
 FEBS Lett. 487 (1), 76-81 (2000)

TITLE
 JOURNAL MEDLINE 20584723
 PUBMED 1152888
 REFERENCE 3 (bases 1 to 1094)
 Genoscope.
 Direct Submission
 Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

QY 214 GYGLYGLUThrleupheglnGlyAenThrAlaProThrAlaAlaGlyLysGlyAla 233
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 DB 1381 ACCAGCTTGGT---GCAGAGCTGGCACTAGAGAGGCTTGGCTGGTAACTG----- 1431
 QY 254 GUGLYAenThrIleGlyAlaThrGlyThrValSerHisSerAlaIleAspLeuGlyThr 273
 DB 1432 ---GGCACCACATACCTGTTGGTGGCACA-----CTTGGCACT 1467
 QY 274 SerAlaIleIleThr---AlaLeuArgAlaAlaGlnGlyHisThrIleTyrrPheTyraP 292
 DB 1468 GGTGAGCGCTTAGTGAAGCTTCAACATGGCAATGGCTTGGC----- 1512
 QY 293 ProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsnIleAsnSerProAsp 312
 DB 1513 -----ATGGGCTTAAAT 1524
 QY 313 ThrGlyAspAsnLysGlyThrGlyThrIleValPheSerGlyGlyLysLeuThrGlu 332
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 DB 1876 GGAGAGCAACAGCACTGAGGTG---GCTTGGAGAGAC 1909
 RESULT 6
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 DEFINITION clone CS0D1005YD03 5-PRIME, mRNA sequence.
 ACCESSION AL543791
 VERSION AL543791
 KEYWORDS EST, GI:31265637
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1022)
 AUTHORS Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12876270.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 10829.f For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D1005CB020P1&cluster=10829.f. Contact :
 Feng Liang Email : fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Paraday Avenue Genoscope sequence ID : CS0D1005B02QP1.
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 /issue_type="PLACENTA COT 25-NORMALIZED"
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 /note="1st strand cDNA was primed with a NotI-oligo(dT)
 primer. Five prime end enriched, double-strand cDNA was
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 sites of the pCMVSPORT 6 vector. Library was normalized."
 BASE COUNT 195 a 282 c 277 g 265 t 3 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 8,02e-05 Length: 1022
 Score: 150.50 Matches: 86
 Percent Similarity: 40.43% Conservative: 45
 Best Local Similarity: 26.54% Mismatches: 104
 Query Match: 3.50% Indels: 89
 DB: 9 Gaps: 15
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 DB 159 AGTTTAAAGTGGCCCACTGACACAGAGTGCACCTTCAAGTGTGAGACCACTGCTGCTTT 218
 QY 37 AspGlyThrThrSerThrThrSer----- 44
 DB 219 GGAGGCACTGACGACCAACGAGCTGGCTTAAAGTGTGACTGACGACTGACCACTTT 278
 QY 45 -----PheSerLysThrSerSerAlaThrAspGly 55
 DB 279 GGCAGTGCACCAACAGACGACGACGCTTCAAGTAGGCGCTTAAAGCAACGACT---GGC 335
 QY 56 ThrAsnTyrrValPheLysAspSerValIleGluAsnValProLysThr----- 72
 DB 336 TTGGAGGCAATCTACGACAGAGTGTCTTTGGTGGTGTCTCCAGCTCCAGCTGAGTAGC 395
 QY 73 ---GlyGlnThrGlnSerThrSer---CysPheLysAsnAspAlaAlaAlaGlyAspLeu 90
 DB 396 TTGGTGTGTACACTGATGATCAGTATCTGCTTC----- 428
 QY 91 AsnPheLeuGlyGlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThrAlaSer 110
 DB 429 -----GGTGGCTCTCCCTGACACAGACGCTGGCTTGGAGGCACTTAGCACC 476
 QY 111 GlyAlaAlaIleGly-----SerGlnAlaAlaAsnLysThrValThrLeuSerGly 127
 DB 477 AGTGTCTCTTGGTGGCTCTTCCAGCACAGGCGCAATTTGGTGTGATCACTAACT--- 533
 QY 128 PheSerAlaLeuSerPheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAla 147
 DB 534 ---ACCAGATCTGCTTATAGCTCTCCAGACAGCTGCTGGCTTGGT---GGTGTCT 587
 QY 148 IleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsn 167
 DB 588 CTCACACACAGTGCACGCTTGGC-----AGTGTGCTC-----AAC 623
 QY 168 PheSerThrGlyAspGlyAlaIleAsnCybalGly-SerLeuLysIleAlaAsnAs 187
 DB 624 ACCAGTACTGTTGGTGTGCTTAAAGACACACAGCTGACTTGGCGGTACACTAACG 683

QY 299 SerThrSerValAlaAspAlaLeuAenlleAsnSerProAspThrGlyAspAsnLysGlu 318
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 QY 319 TyrThrGlyThrIleValPheSerGlyGluValLeuThrGluAglValAlaLysAspGlu 338
 DB 661 TTCTCATCTCTTCTCCATTCGCGCCGAGCAGAGTATCGTCCGCC----- 617
 QY 339 LysAsnArgThrSerLysLeuLeuGlnAenValAlaPheLysAsnLysThrValValLeu 358
 DB 616 -----TTGTCGAGCCTTCTCAGCGTCATCATCAGTTTCAGTA 581
 QY 359 LysGlyAspValValLeuSerAlaAenGlyPheSerGlnAspAlaAsnSerLysLeu 378
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 QY 379 MetAspLeuGlyThrSer 384
 DB 523 TCTTCACTTGCGGCGCTCC 506

RESULT 8
 LOCUS BX405896 1164 bp mRNA linear EST 13-MAY-2003
 DEFINITION BX405896 Homo sapiens FETAL LIVER Homo sapiens CDNA clone
 ACCESSION CS0DM009YB14 5-PRIME, mRNA sequence.
 VERSION BX405896
 KEYWORDS BX405896.1 GI:30635433
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 1164)
 Li,W.B., Gruber,C., Jessee,J. and Polyses,D.
 Full-length cDNA libraries and normalization
 Unpublished
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 10458.T, and
 it belongs to a clone representative of this cluster. For more
 information about this cluster and the virtual cDNA, see
 http://www.genoscope.cns.fr/Contact : Feng Liang Email :
 fliang@lifeitech.com URL : http://fulllength.invitrogen.com/
 Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID :
 CS0AM009BC070P1.

FEATURES
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 /note="Organ: liver; Vector: PCWSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the PCWSPORT 6
 vector. Library was not normalized."
 BASE COUNT 297 a 277 c 307 g 237 t 46 others
 ORIGIN

Alignment Scores:
 Pred. No.: 0.000472 length: 1164
 Score: 144.00 Matches: 79
 Percent Similarity: 40.21% Conservative: 38
 Best Local Similarity: 27.15% Mismatches: 94
 Query Match: 3.35% Indels: 80
 DB: 13 Gaps: 15

US-09-830-446-27 (1-841) x BX405896 (1-1164)
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 DB 835 GGGCCAGCTTAGTGAGTGGAGTACAGTCTGTTTAGTGGCCACTCAGACCCAGTGC 776
 QY 27 ThrGluLeuSerAlaSerAsnSerPheAspGlyThrThrThrThr 44
 DB 775 ACTTTCAGTGGGAGCCAGCTCTGCTTGGAGGACACTGACACCCAGGCTGCTT 716
 QY 45 -----Phe 45
 DB 715 AGTGTGACTCAGAACTAGACACAGATTGGCAGTGCACCCAGACGAACTCTTC 656
 QY 46 SerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPheLysAspSerVal 65
 DB 655 AGTATGTGCGCTTAGACCACTAAGT---GGCTTGGAGGATCTAGCAGCAGCTGTCT 599
 QY 66 IleGluAsnValProLysThr-----GlyGluThrGlnSerThrSer---Cys 80
 DB 598 TTTGGTGCTCTCCAGCTCCAGCTCAGTGTGCTTGGTGTGACTGATCCAGTATCTCC 539
 QY 81 PheLysAsnAspAlaAlaIaGlyAspLeuAsnPheLeuGlyGlyPheSerPheThr 100
 DB 538 TTC-----GTTGGCTCTCCCTGCAC 518
 QY 101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGly-----SerGlu 117
 DB 517 AGNACTGCTTGGAGGACACTTAGCACAGTGTCTCTTGGTGTGCTTCCAGCAC 458
 QY 118 AlaAlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerPro 137
 DB 457 AGTGCATATTTGGTGGTGTACCTAAGT-----ACGAGATCTGCTTTATAGTCTTCCC 404
 QY 138 AlaSerThrValThrAsnGlyLeuGlyAlaIaAsnValLysGlyAsnLeuSerLeu 157
 DB 403 AGAAGTGTGCTGCTGCTTGGT---GTTGCTTCACACAGTCCAGCTTGGC----- 353
 QY 158 AspAsnAspLysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsn 177
 DB 352 -----AGTGTCTC-----AACACAGTACTGCTTTGGTGTGCTATGAGC 311
 QY 178 CysAlaGlySerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGly----- 194
 DB 310 ACCAGTGTGACTTTGGCGGTACCTAGACACAGTGTGCTTTGGTGTGCTCTCTGCGC 251
 QY 195 -----AsnSerSerSerThrArgGlyGlyAlaIleHis 205
 DB 250 ACCAGTGTGACTTTGGCAGTGCAGTCAACACCAATGCTGTTATGTGTGCTGTCTGAC 191
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 DB 190 ACCAAGTGTGACTTTGGTGTGCTAGTCAAGACCC-----AGGCTGTGTTGGTGTGC 140
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 QY 243 SerLeuSer-----GlyAspSerGlyAspLeu 251
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 DEFINITION Yarrowia lipolytica, genomic survey sequence.
 ACCESSION AL414226 GI:12187157
 VERSION AL414226.1
 KEYWORDS GSS.
 SOURCE Yarrowia lipolytica
 ORGANISM Yarrowia lipolytica
 BUKARYOTA; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

REFERENCE
AUTHORS
1 (bases 1 to 977)
Soucier,J.L., Aigle,M., Attienave,P., Blandin,G.,
Boloetin-Pukhara,M., Bon,E., Brottier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durieux,P., Lepingle,A., Morente,B.,
Malpertuy,A., Neveuglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekala,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
FEMS Lett. 487 (1), 3-12 (2000)
20584711
1152876
2 (bases 1 to 977)
Casaregola,S., Neveuglise,C., Lepingle,A., Bon,E., Feynrol,C.,
Attienave,P., Wincker,P. and Gaillardin,C.
Genomic exploration of the hemiascomycetous yeasts: 17. Yarrowia
lipolytica
FEMS Lett. 487 (1), 95-100 (2000)
20584727
1152892
3 (bases 1 to 977)
Genoscope.
Direct Submission
Submitted (07-SRP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
seqreg@genoscope.cns.fr - Web : www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxi,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
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keywords for description of this sequence and for the sequence of
the other extremity of this insert.
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misc_feature
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US-09-830-446-27 (1-841) x CNS06T8C (1-977)
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Gy 49 ThrSerSerAlaThrAspelyThrAsnlyrValAlPheIysAspSerValValIleGlu 68
Db 89 TcTcTCTCCGCTCTCTCTCTCTCTCTGCGGCTGTGGAGATCTCTCA-----ACT 136
Gy 69 ValPProlyrThrGlyGluThrGlnSerThrSerCySPheIysAsnAspAlaIalAlaGly 88
Db 137 ACAGGTGCTGCTGGAGAGTCTCTTACTACT-----GCGGTGCTGGC 178

Oy		89	AapLeuaanPhaeleuglygyl---GlyPheSerPheThrPheSerAenile---AspAla	106
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Oy		107	ThtThralaserglyalaaalaaleglySerglu-----AlaalaaenlysrthaValThr	124
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Oy		125	LeuSerGlyPheSerAlaleuSerPheLeuLySerProla---SerThraValThrAan	143
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DEFINITION	T7 end of clone BBOAA0010q4 of library BBOAA from strain CBS 4732			
ACCESSION	AL431075 genomic survey sequence.			
VERSION	AL431075.1 GI:12214487			
KEYWORDS	GSS,			
SOURCE	Pichia angusta			
ORGANISM	Pichia angusta			
REFERENCE	Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;			
AUTHORS	Saccharomycetales; Saccharomycetaceae; Pichia.			
	1 (bases 1 to 1159)			
	Souciat,J.L., Aigle,M., Attiguenave,F., Blandin,G.,			
	Boclot,H.,Fukuhara,M., Bon,E., Broctier,P., Casaregola,S.,			
	de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,			

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
 Plate: LLM14077 row: k column: 24
 High quality sequence start: 22
 High quality sequence stop: 703.
 Location/Qualifiers

1. 1001

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 NotI; cloned unidirectionally. Primer: Oligo dT. Average
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 Corp. Note: this is a N1H MGC library."

BASE COUNT 196 a 255 c 276 g 272 t 2 others

ORIGIN

Alignment Scores:

Pred. No.:	0.000685	Length:	1001
Score:	141.50	Matches:	79
Percent Similarity:	36.57%	Conservative:	34
Best Local Similarity:	25.57%	Mismatches:	105
Query Match:	3.29%	Indels:	91
DB:	13	Gaps:	14

US-09-830-446-27 (1-841) x BQ963411 (1-1001)

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Oy 30 LeuSerAlaSerAenSerPheAapGlyThrThrSerThrThrSerPheSerSerlyThr 49
Db 24 CTCACCAACAACACAGCTTGGCGAGTGACACCACTACAGACAGCTTGCAGTGTGCA 83
Oy 50 SerSerAlaThrAapGlyThrAenTyValPheLyAapSerValValIleGluAenVal 69
Db 84 GTTACTACACCACTGGC-----
Oy 70 ProLyThrGlyGluThrGlnSerThrSer---CysPheLyAenAapAlaAlaIleGly 88
Db 102 -----TTTGAAGGACACTTACACAGCTGCTGCTTT-----GCT 137
Oy 89 AspLeuAenPheLeuGlyGlyGlyPheSerPheThrPheSerAenIleAapAlaThrThr 108
Db 138 AGTCTCCCTACTCTGGCGCTGGCTTTGGAGGACACCTTAACT--
Oy 109 AlaSerGlyAlaAlaIleGlySerGluAlaAlaAenLyThrValThrLeuSerGlyPhe 128
Db 179 -----
Oy 129 SerAlaLeuSerPheLeuLySerProAlaSerThrValThrAenGlyLeuGlyAlaIle 148
Db 180 ACCAGATCTCTCTTGGTGGCTTCTCTACAC-----AATACGTGTTTGGT----- 227
Oy 149 AenVallyGlyAenLeuSerLeuAenAapLyValIleIleGlnAapAenPhe 168
Db 228 -----GGTACACTAGC-----ACCAGTCTTCTCTGGCTCTTCTCT 266
Oy 169 SerThrGlyAap-----GlyGlyAlaIleAenCysAlaGlySerLeuLyIleAlaAen 186
Db 267 AGCACACACTCTGACTTGTGGTGACACTAACACACTAGTCACTTGGCTGGCTCTCT 326
Oy 187 AenLySerLeuSerPheIleGly-----AenSerSerSerThrAenGlyGlyAlaIle 204
Db 327 GGTGCATATGCTGGCTTGGCGGTACACTACACAGAGTACACAGCTTGGCGGTGCATC 386
Oy 205 HisThrLyAenLeuThrLeuSerSerGlyGlyGlyThrLeuPheGlnGlyAenThrAla 224
Db 387 AGCAC-----AGCACTGGC-----TTTGGACAGTGACATC 416

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Oy 225 ProThrAlaAlaGlyLyGlyGlyAlaIleAlaIleAlaAapSerGlyThrLeuSerIle 244
Db 417 AATAACAGTGCACACTTTGGTGGTGCCATGATACCAAGCTTATGATGATCAATAGC 476
Oy 245 SerGlyAapSerGlyAapIleIlePheGluGlyAenThrIleGlyAlaThrGlyThrVal 264
Db 477 AGTCCACAGCTTGTGGTGGCTATC-----AACACAGTGGTGGCTTGGCAGATCA 527
Oy 265 SerHisSerAlaIleAapLeuGlyThrSerAlaLyIleThrAlaLeuAlyAlaGln 284
Db 528 CTCACACAGACAGTGCACCTTGGCAGTGACCTACAGCACAGTGCACCTTGGTGT--- 584
Oy 285 GlyHisThrIleTyThrPheTyAapProIleThrValThrGlySerThrSerValAlaAap 304
Db 585 -----GTACTCAATGCGAGTGGCTGCTTGGTGT 614
Oy 305 AlaLeuAenIleAenSerProAapThrGlyAapAenLyGlyTyThrGlyThrIleVal 324
Db 615 GCTTGAACACCATGCGACCTTGGTGT-----GTACTCAATGCGAGTGGTGGC 665
Oy 325 PheSerGlyGlyLyLeuThrGlyAla 333
Db 666 TTGTGTGGTGCATGACCAATGCC 692

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RESULT 12

BE583883

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CONTACT: Gijzen M

AGRI-CULTURE and AGRI-FOOD Canada

1391 Sandford Street, London, Ontario, Canada N5V 4T3

Tel: 519 457 1470

Fax: 519 457 3997

Email: gijzenm@em.agr.ca

Transcript obtained from mixed plant-pathogen interaction culture.

FEATURES

source

1. 634
 /organism="Glycine max/Phytophthora sojae mixed EST
 library"
 /mol_type="mRNA"
 /strain="Phytophthora sojae race 2 strain P6497"
 /cultivar="Glycine max cultivar Harosoy"
 /db_xref="taxon:135715"
 /tissue_type="Plant hypocotyls infected with Phytophthora
 sojae"
 /dev_stage="8 d old etiolated hypocotyls 48 h
 post-inoculation with Phytophthora sojae zoospores"
 /lab_host="E. coli strain XL04R"
 /clone_1lb="PsojaeHA"
 /note="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI; This
 cDNA library was constructed from polyA+ enriched mRNA
 from etiolated hypocotyls 48 h post-inoculation with
 Phytophthora sojae zoospores. Complementary DNA was
 synthesized from mRNA using an XhoI-poly(dT)
 linker-primer. EcoRI adapters were ligated to the
 blunt-ended cDNA fragments and the products were digested
 with XhoI for directional cloning into lambda ZAP Express
 vector. This lambda library was amplified once using E.
 coli host strain XL1 Blue MRF'. Inserts were then

subcloned by mass excision using Exaseist helper phage
for conversion into phagemid vector pBK-CMV in E. coli
host strain XL10R. Sequenced using T3 primer: 5' ATT AAC
CCT CAC TAA AGG GA 3'.

BASE COUNT 146 a 227 c 182 g 78 t 1 others
ORIGIN

Alignment Scores:

Pred. No.:	Length:	634
Score: 0.000434	Matches: 66	
Percent Similarity: 140.50	Conservative: 35	
Best Local Similarity: 23.08%	Mismatches: 94	
Query Match: 3.27%	Indels: 91	
	Gaps: 13	

US-09-830-446-27 (1-841) x BE583883 (1-634)

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QY 31 SerAlaSerAanSerPheAapGlyThrThrSerThrSerPheSerSerlyThrSer 50
DB 6 ACCGCGACCAACTCT-----GGTACCTCGACCAACGACCTCGGTCACGACTTCG 59
QY 51 SerAlaThrAapGlyThrAanTyTrValPheIlyAapSerValIleGluAanValPro 70
DB 60 ACCACCAACCGCGCGGCACTAC-----
QY 71 LysThrGlyIleThrGlnSerThrSerCySPheIlyAanAapAlaIleAglAapLeu 90
DB 81 AGCTCCGGACCACTTCCTCCTCCTACGAGGAAACACGACTCGGTCACGACTTCGACC 140
QY 91 AamPheLeuGlyIleGlyIlePheSerPheThrPheSerAanIleAapAlaThrThrAlaSer 110
DB 141 AAC-----TCTGTACGACCTCGACTCGACTCGACCAACGCGGCAACGACGACTCC 191
QY 111 GlyAlaAlaIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 130
DB 192 GGT-----ACGACTTCCTCCACCAACGACCACTCGGCGACGCTCCACC 230
QY 131 LeuSerPheLeuIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 150
DB 231 ---TCAACGACGACCGCGCGGCACTCGACCACTCGACCGGCG----- 269
QY 151 LysGlyAanLeuSerLeuLeuAanAapIlyValIleIleGlnAapAanPheSerThr 170
DB 270 -----CAGCGACGACGCGGCACTCG----- 287
QY 171 GlyAapGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 187
DB 288 GGTCCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 335
QY 188 LysSerLeuSerPheIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 207
DB 336 GAGACGACAT-----ACGACTTCACCAACGCGGCTCGACGCGGCAACGACGATC 380
QY 208 AamLeuThrLeuSerSerGlyIleIleIleIleIleIleIleIleIleIleIleIleIle 227
DB 381 AGCAGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 425
QY 228 AlaGlyIleGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 247
DB 426 ACGGCTTCGCGGCTCGCTGTCGTCGACGACGACGACGACGACGACGACGACGAC 467
QY 248 SerGlyAapIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 267
DB 468 -----GGCGGCTCCATTGAGACCAACGACGACGACGACGACGACGACGACGAC 494
QY 268 AlaIleAapLeuGlyIleThrSerAlaIleIleIleIleIleIleIleIleIleIleIle 287
DB 495 -----GGCTCCGAGGACGACGACGACGACGACGACGACGACGACGACGACGACGAC 542
QY 288 IleTyPheTyThrAapProIleThrValIleGlySerThrSerValIleAapAlaLeuAan 307
DB 543 -----ACTACGACGACGCGGACGACGACGACGACGACGACGACGACGACGACGAC 581

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QY 308 IleAanSerProAapThr 313
DB 582 TCTGGCAACCCACGACACT 599

RESULT 13

CA318878 779 bp mRNA linear EST 26-NOV-2002
LOCUS CA318878
DEFINITION UI-M-FMO-cbr-1-23-0-UI r1 NIH_BMAP_FMO Mus musculus cDNA clone
IMAGE: 6813528 5', mRNA sequence.
ACCESSION CA318878
VERSION CA318878.1 GI:24537002
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE NIH-MGC http://mgs.nci.nih.gov/.
AUTHORS 1 (bases 1 to 779)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/BLN at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pyx-5
Location/Qualifiers

1..779
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE: 6813528"
/cruise_type="Whole Brain"
/dev_stage="embryo 13.5, 14.5, 16.5, 17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_11b="NIH BMAP_FMO"
/note="Organ: Brain; Vector: pyx-Aac; Site_1: Ecor I;
Site_2: Not I; The library was constructed according
to Bonaudo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into pyx-Aac vector. The library tag
sequence located between the Not I site and the polyA tail
is ACCGAGACG. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemlin Chin, Ph.D.,
program coordinator."

BASE COUNT 154 a 209 c 203 g 212 t 1 others
ORIGIN

Alignment Scores:

Pred. No.:	Length:	779
Score: 0.000671	Matches: 80	
Percent Similarity: 140.00	Conservative: 38	
Best Local Similarity: 25.89%	Mismatches: 108	
Query Match: 3.26%	Indels: 83	
	Gaps: 15	

US-09-830-446-27 (1-841) x CA318878 (1-779)

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QY 31 SerAlaSerAanSerPheAapGlyThrThrSerThrSerPheSerSerlyThrSer 50
DB 60 ACCACCAACCGCGCGGCACTAC-----

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Db 501 CCATCAACAAACAGGTGATTATTGGAGCACTACACAGCACTACAGCAACAAACA 560
 QY SerIleSerGly-----AaspSerGlyAaspIle 251
 Db 561 ACAACAGTGGATTATTGGCGGATCTCAACACACCATCATTAACAGTGGAGGT 620
 QY 252 IlePheGluGlyAanthrIleGlyAlaThrGlyThrValSerHisSerAlaIleAaspLeu 271
 Db 621 TTAATTGGAGCACTACACAGGAGCTACAAACAAACAAACATCTCAGCTATACATCA 680
 QY 272 GlyThrSerAlaIleThrAlaLeuArgAlaAlaGlnGlyHisThrIleTyrPheTyr 291
 Db 681 TTAACCTACC-----GGAGGAGAGGTATTATTGGAN 710
 QY 292 AspProIleThrValThrGlySerThrSerValAlaAaspAlaLeu---AanIleAanSer 310
 Db 711 GGATCTACACATCAACCATCATTAATGAGGAGGATTATTGGAGCAACATCAACCAAN 770
 QY 311 ProAaspThr 313
 Db 771 CCANCTACA 779

RESULT 15
 CD284689/c 698 bp mRNA linear EST 23-MAY-2003
 LOCUS G39178.95 NCI_CGAP_ZK1d1 Dantio rerio cDNA clone IMAGE:524567 5',
 DEFINITION mRNA sequence.
 ACCESSION CD284689
 VERSION CD284689.1 GI:31062465
 KEYWORDS EST.
 SOURCE Dantio rerio (zebrafish)
 ORGANISM Dantio rerio
 Baktayocae; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
 ; Cyprinidae; Danio.
 Amundsen, C., Cachuela, N., Chen, F., Cheung, L.M., Chong, A., Murray, L.,
 Oliva, J., Park, C., Reyes, J., Yungen, J. and Swimmer, C.
 1 (bases 1 to 698)
 Expressed sequence tags from NCI_CGAP_ZK1d1, a Dantio rerio kidney
 library
 JOURNAL Unpublished
 COMMENT Contact: Chen F.
 Exelixis, Inc.
 170 Harbor Way, PO Box 511, South San Francisco, CA 94083-0511, USA
 Tel: 650 837 7000
 Fax: 650 837 8300
 Email: fchen@exelixis.com
 DNA sequencing by: Exelixis, Inc. Clone distribution information
 can be found through the I.M.A.G.E. Consortium/ILMIL at:
 http://image.llnl.gov
 Plate: 1416 row: N column: 23
 High quality sequence stop: 698.
 Location/Qualifiers
 1..698
 source
 /organism="Dantio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:524567"
 /lab_host="DH10B (71-resilient)"
 /note="Organ: Kidney; Vector: pCMV-SPORT6, ccdb; Site: 1;
 EcoRV; Site 2: NotI; Cloned unidirectionally. Primer:
 Oligo dT. Average insert size 1.8 kb. Constructed by J.
 Wang (Research Genetics, Invitrogen Corp) from tissue
 donated by L. Zon (Harvard University). Note: this is a
 NCI_CGAP library."

BASIS COUNT 226 a 186 c 182 g 104 t
 ORIGIN

Alignment Scores:
 Pred. No.: 0.00168 Length: 698
 Score: 135.50 Matches: 79
 Percent Similarity: 35.74% Conservative: 30

Best Local Similarity: 25.90% Mismatches: 103
 Query Match: 3.15% Indels: 93
 DB: 14 Gaps: 15

US-09-830-446-27 (1-841) x CD284689 (1-698)

QY 25 AlaThrThrGluGluLeuSerAlaSerAanSerPheAaspGlyThrThrSerThrThrSer 44
 Db 698 TCTACTACTCTCCCTGCTGAGCTGTTCTTCACTGAGGAGCTGCAAGTGAAGTGAAGTGA 639
 QY 45 PheSerSerIleThrSerSerAlaThrAaspGlyThrAanTyrValPheIleAaspSerVal 64
 Db 638 GGCTCTCAGAGCTCAGTGCAGCATCTCAGGTCACACT-----GCAGATTCC-- 591
 QY 65 ValIleGluAanValProIleThrGlyGluThrGlnSerThrSerCysPheIleAanAap 84
 Db 590 -----TCAGCTTCAGGGGAGGAGCTGTCCTTCA-----GGT 558
 QY 85 AlaAlaAlaGlyAaspLeuAanPheLeuGlyGlyPheSerPheThrPheSerAanIle 104
 Db 557 GCAGCAGCAGGTGCTTCTTCC---ACTGCTGATGAAATCTCAGAAAGTGTACAGGTCC 501
 QY 105 AaspAlaThrThrAlaSerGlyAlaAlaIleGlySerGlu----- 117
 Db 500 TCTGCACATGTCCTTCTGCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 441
 QY 118 -----AlaAlaAanIleThrValThrLeuSerGlyPheSerAlaLeu 131
 Db 440 TTAACGTGTCTCAGAGCAGCAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 387
 QY 132 SerPheLeuIleSerProAaspThrValThrAanGlyLeuGlyAlaIleAanValIys 151
 Db 386 -----ATACACGTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 333
 QY 152 GlyAanLeuSerLeuLeuAanAaspIleValIleGlnAaspAanPheSerThrGly 171
 Db 332 GCTGGTCTTCA-----GGTTTTTAACGTGT 306
 QY 172 AaspGlyGlyAlaIle-----AanCysAlaGlySerLeuIleAlaAanAanIys 188
 Db 305 GACTCTGTCAGCTGTCAGCTGCTCCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 255
 QY 189 SerLeuSerPheIleGlyAanSerSerSerThrArgGlyAlaAlaIleHisThrIysAan 208
 Db 254 -----GCAGGCTCTGCGACACTGTCAGCTGCT----- 225
 QY 209 LeuThrLeuSerSerGlyGlyLeuThrLeuPheGlnGlyAanThrAlaProThrAlaAla 228
 Db 224 -----TCTGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCA 177
 QY 229 GlyIleGlyGlyAlaIleAlaIleAaspSerGlyThrLeuSerIleSerGlyAaspSer 248
 Db 176 -----GCTGGGCGCTTTGTGTAGCA----- 156
 QY 249 GlyAaspIleIlePheGluGlyAanThrIleGlyAlaThrGlyThrValSerHisSerAla 268
 Db 155 -----GCTGTTCTCTTACTGCTGCT 135
 QY 269 IleAaspLeuGlyThrSerAlaIleThr-----AlaLeuArgAlaAlaGlnGlyHis 286
 Db 134 GCAAGATGCTGATACGCTGCTGATGCTGATGCTGAGGACATGCTGCTGCTGCTGCTGCTGCT 75
 QY 287 ThrIleTyrPheThrAaspProIleThrValThrGlySerThrSerValAlaAaspAlaLeu 306
 Db 74 GGAGTAGATGTC-----TCTGTGTGTCACGTGCTTCTTCAAGTGCACATCATCTCTTC 21
 QY 307 AanIleAanSerPro 311
 Db 20 ---TTTACTCTTCT 9

Search completed: January 29, 2004, 17:50:08
 Job time : 4279 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 29, 2004, 10:21:11 / Search time 121 Seconds
(without alignments)
3067.795 Million cell updates/sec

Title: US-09-830-446-27

Perfect score: 4295
Sequence: 1 MKIPLRFLILSVPTLSMSN.....FEWRGSSRSYNDAGSKIRF 841

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Db=Issued_Patents_NA -OPMT=faetap -SUFITX=p2n.rn1 -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTPMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSFBLOCK=100 -LONGIOG
-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: Issued Patents_NA.*
- 2: /cgsm2_6/ptodata/1/ina/5A.COMB.seq.*
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- 6: /cgsm2_6/ptodata/1/ina/BACKFILE1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4255	99.1	1230025	4	US-09-198-452A-1
2	1365	31.8	1230025	4	US-09-198-452A-1
3	939	21.9	3021	4	US-09-556-877-182
4	939	21.9	3021	4	US-09-620-412C-182
5	939	21.9	3021	4	US-09-598-419-182
6	936	21.8	2949	4	US-09-556-877-170
7	936	21.8	2949	4	US-09-620-412C-170
8	936	21.8	2949	4	US-09-598-419-170
9	711.5	16.6	2643	4	US-09-556-877-169
10	711.5	16.6	2643	4	US-09-620-412C-169
11	711.5	16.6	2643	4	US-09-598-419-169
12	696.5	16.2	2601	4	US-09-556-877-181

13	696.5	16.2	2601	4	US-09-620-412C-181	Sequence 181, App
14	696.5	16.2	2601	4	US-09-598-419-181	Sequence 181, App
15	527.5	12.3	2895	4	US-09-556-877-171	Sequence 171, App
16	527.5	12.3	2895	4	US-09-620-412C-171	Sequence 171, App
17	527.5	12.3	2895	4	US-09-598-419-171	Sequence 171, App
18	527.5	12.3	2934	4	US-09-556-877-183	Sequence 183, App
19	527.5	12.3	2934	4	US-09-620-412C-183	Sequence 183, App
20	527.5	12.3	2934	4	US-09-598-419-183	Sequence 183, App
21	506	11.8	5265	4	US-09-556-877-174	Sequence 174, App
22	506	11.8	5265	4	US-09-620-412C-174	Sequence 174, App
23	506	11.8	5265	4	US-09-598-419-174	Sequence 174, App
24	447.5	10.4	5331	4	US-09-556-877-173	Sequence 173, App
25	447.5	10.4	5331	4	US-09-620-412C-173	Sequence 173, App
26	447.5	10.4	5331	4	US-09-598-419-173	Sequence 173, App
27	433	10.1	4593	4	US-09-556-877-172	Sequence 172, App
28	433	10.1	4593	4	US-09-620-412C-172	Sequence 172, App
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30	430.5	10.0	2547	4	US-09-556-877-184	Sequence 184, App
31	430.5	10.0	2547	4	US-09-620-412C-184	Sequence 184, App
32	430.5	10.0	2547	4	US-09-598-419-184	Sequence 184, App
33	421	9.8	2847	4	US-09-556-877-186	Sequence 186, App
34	421	9.8	2847	4	US-09-620-412C-186	Sequence 186, App
35	421	9.8	2847	4	US-09-598-419-186	Sequence 186, App
36	341	7.9	2103	4	US-09-620-412C-344	Sequence 344, App
37	341	7.9	2103	4	US-09-598-419-344	Sequence 344, App
38	333	7.8	2076	4	US-09-620-412C-312	Sequence 312, App
39	333	7.8	2076	4	US-09-598-419-312	Sequence 312, App
40	290	6.8	2148	4	US-09-620-412C-328	Sequence 328, App
41	290	6.8	2148	4	US-09-598-419-328	Sequence 328, App
42	266	6.2	1965	4	US-09-620-412C-340	Sequence 340, App
43	266	6.2	1965	4	US-09-598-419-340	Sequence 340, App
44	266	6.2	2052	4	US-09-620-412C-356	Sequence 356, App
45	266	6.2	2052	4	US-09-598-419-356	Sequence 356, App

ALIGNMENTS

RESULT 1
US-09-198-452A-1
Sequence 1, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment thereof and uses thereof, in particular for the diagnosis, prev
TITLE OF INVENTION: and treatment of infection
FILIR REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1
LENGTH: 1230025
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(15000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (15001)..(30000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (30001)..(45000)
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LOCATION: (45001)..(60000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (60001)..(75000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (75001)..(90000)
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OTHER INFORMATION: -na or c or g or t
NAME/KEY: misc_feature
LOCATION: (465001)..(480000)
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 OTHER INFORMATION: n=a or c or g or t
 NAME/KEY: misc_feature

Alignment Scores:

Pred. No.:	0	Length:	1230025
Score:	4255.00	Matches:	840
Percent Similarity:	99.76%	Conservative:	0
Best Local Similarity:	99.76%	Mismatches:	1
Query Match:	99.07%	Indels:	2
DB:	4	Gaps:	0

US-09-830-446-27 (1-841) x US-09-198-452A-1 (1-1230025)

QY 1 MetIyAlEProLeuArpPheLeuLeuIleSerLeuValProThrLeuSerMetSerAa 20
 Db 28950 ATGAAGATTCACCTCCGCTTTTATGATATCATTTAGTACTGCTTCTTCTGAT 29009
 QY 21 LeuLeuGlyAlAlaThrThrGluGluLeuSerAlSerAaSerPheAapGlyThrThr 40
 Db 29010 TTATTAAGAGCTGCTCTACCGAAGAGTTATCCGCTAGCAATGCTTCATGGAACCTACA 29069
 QY 41 SerThrThrSerPheSerSerLyThrSerSerAlaThrAapGlyThrAaThrValPhe 60
 Db 29070 TCACACACAGCTTCTCTGTAACACATCATCGCTACAGATGGACCAATTAATGTTTT 29129
 QY 61 LyAaSPSerValAlaIleGluAaAValProLyThrGlyGluThrGlnSerThrSerCys 80
 Db 29130 AAAGATTCCTGATGTTATAGAAATGTAACCAAAACAGGGAAACTAGCTACTACTTGT 29189
 QY 81 PheLyAaAaSPAlAlaAlaAglAaPLeuAaAaPheLeuGlyGlyPheSerPheThr 100
 Db 29190 TTTAAATAAGACCTGCTGACGTGAGATCTAAATTTCTTAGAGGGGGAATTTCTTCACA 29249
 QY 101 PheSerAaAaSPAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAaAaAa 120
 Db 29250 TTTAGCAATATGATGATCAACACAGGCTTCTGAGCTGCTAATGGAAGTAAAGACGTAAT 29309
 QY 121 LyThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLySerProAlaSerThr 140
 Db 29310 AAGACGTCACGTTATACAGATTTTCGACCTTTCTTTCTTAAATCCCAAGCAATACA 29369
 QY 141 ValThrAaGlyLeuGlyAlaIleAaAaValLyGlyAaAaLeuSerLeuAaAaAaP 160
 Db 29370 GTGACATTAAGGATTTGGAGCTATCAATGTTAAAGGAATTTAAGCTAATGATATGAT 29429
 QY 161 LyValAlaLeuIleGluAaAaAaPheSerThrGlyAaGlyGlyAlaIleAaCysAlaGly 180
 Db 29430 AAGGATTAATATTCAGCAATTTCTCAACAGAGAGAGGCGGACA-ATTAAATGTCGAGCC 29488
 QY 181 SerLeuLyAlAlaAa 200
 Db 29489 TCTTGAAGATTCGCAACATTAAGTCCCTTTCTTTATTTGAAATAGTTCTTCAACACT 29548
 QY 201 GlyGlyAlaIleIleThrLyAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 220
 Db 29549 GCGGAGCAATTCATCAACAAAACCTCACATATCTTGTGGGGAAACCTAATTTTCAG 29608
 QY 221 GlyAaThrAlaProThrAlaAlaGlyLyGlyGlyAlaIleAlaIleAaSPSerGly 240
 Db 29609 GGGATACAGCCCTTACCGCTGTGTAAAGAGGTGCTATCCGATTTGCACACTCTGCG 29668
 QY 241 ThrLeuSerIleSerGlyAaSPSerGlyAaPheIleIlePheGluGlyAaThrIleGlyAla 260
 Db 29669 ACCCTATCCATTTCTGAGACAGTGGCGACATATATCTTTGAAGGCAATACGATAGAGCT 29728
 QY 261 ThrGlyThrValSerThrSerAlaIleAaPLeuGlyThrSerAlaLyIleThrAlaLeu 280
 Db 29729 ACAGGAACCGTCTCTCATATGCTCTAATTTAGTAAGAACTAGGCTTAAGTAATCTGGTTA 29788
 QY 281 ArgAlaAlaGlyGlyIleThrIleThrPheThrAaSPProIleThrValThrGlySerThr 300
 Db 29789 CCGTCTGCGCAAGACATACGATATACCTTTATGATCCATTAATCTTAACAGATGACA 29848
 QY 301 SerValAlaAaSPAlaLeuAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 320
 Db 29849 TCTGTTGCTGATGCTCTCAATTAATTAATACCTGATACGAGATACAAAGATTAAG 29908
 QY 321 GlyThrIleValPheSerGlyGlyLyLeuThrGluAlaGluAlaAaAaPLeuAaAa 340
 Db 29909 GGAACCATATGCTCTTTCTGAGAGAAAGCTCACGAGGCGAAGCTTAAGATGAGAAAC 29968
 QY 341 ArgThrSerLyLeuGluGluAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAaAa 360
 Db 29969 CGCACTTCAATATCTTCAAAATGCTGCTTTTAAATAAGGACGTGATTTTGAATAAG 30028
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 Db 30029 TGATGCTGTTTAAGTGCAAGGTTTCTCTCAGATGCAAACTCAATGATTAATGA 30088
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 Db 30089 TTTAGGAGAGCTGCTGTTGTCGCAACACCAAGATTCGATTAAGCAATTTGGAATTA 30148
 QY 400 nIleAaSPSerLeuAa 420
 Db 30149 TATAGCTCTTCAGAGAACGGGAAAGTAATTAACAGTGTCCACAGCTCCAGAAACA 30208
 QY 420 PLeaArgIleAaSPArProValIleAaAaIleSerAaSPGluSerPheTyGlnAaSP 440
 Db 30209 TATGCTATAGATTCGCTCGTGTGATGCTGCAATTAAGCATGAGATTTTATCAAAATG 30268
 QY 440 yPheLeuAaGluAa 460
 Db 30269 CTTTGTGAATGAGACCAATTCATATGATGGATTTCTTGATTAAGATGCTGGAAAGACAT 30328
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 QY 480 yLySerTrpThrIleAa 500
 Db 30389 AAAGTGACAGATCAATGCTGCTACATGATGATTAAGAAAGCTACGCTTTCTGGCGCAAGCA 30448
 QY 500 nSerPheAa 520
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 Db 30509 TTTTATAGATGTCGTTCTCTTCAGAAATTTTAAAGCTAGGATCTGAAGGTCCTCTTA 30568
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 QY 560 nGluAaSPPheAa 580
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QY 580 GGIYGLIAPThrLeuSerLeuGlyPheAlaGluPheAlaArgAspLysAspTyrPh 600
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QY 600 eWeRAnThraPheAlaLysThrTyrAlaGlySerLeuArgLysAlaAspAlaSe 620
| | | | |
Db 30749 TATGAATACCAATTCGCAAGACCTAGCAGAGATCTTACGTTTGAGCAAGATGCTTC 30808
QY 620 rLeuTyrSerValValSerLileuLeuGlyGlyGlyLysLeuArgGlyLileuLeuPr 640
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Db 30809 CCTAATCTCTGAGGATATCTCTTACAGACAGGAGAGACTCCCGAGATCTCTTGCC 30868
QY 640 cTyTAlaSerLysThrLeuProCysSerPheTyrGlyGluLeuSerTyrGlyLysThrAs 660
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature

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Alignment Scores:
Pred. No.: 1,28e-132 Length: 1230025
Score: 1365.00 Matches: 329
Percent Similarity: 51.04% Conservative: 161
Best Local Similarity: 34.27% Mismatches: 320
Query Match: 31.78% Indels: 151
DB: 4 Gaps: 22

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US-09-830-446-27 (1-841) x US-09-198-452A-1 (1-1230025)

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QY 1 MetIvEILPLeProLeuArghPheLeuLeuIle---SerLeuValPProthrIleuSerMetSer 19
DB 518200 ATGAATCGCAATTTCCTGGTAGCTCTTCGACATGTGGCATGTTTACTACTGTG 518141
QY 20 AsnLeuLeuGlyAlaIalathrThrgIuLeuSerAlaSerAsnSerPheaspGlyThr 39
DB 518140 TCCACGTGTTTTCCTGCACTGCTGAAATATAGCCCTCGATGCTTTGACGGAAT 518081
QY 40 ThrSerThrThrSerPheSerSerIythrSerSerAlaThrAspGlyThrAsnIyVal 59
DB 518080 ACTAACACACGACCTATACCTCTTAA-----AAATGACATGAGTAATGACTATACT 518027
QY 60 PheIyAspSerValValIleGluSerValProlYsrThrgIyIuhrGlnSerThrSer 79
DB 518026 CTGACACGAGATATTAATCTGCAAAACCTT-----GGGATTCGGCAGCTTTAAAG 517976
QY 80 -----CyPheIyAsnAspAlaIalagIyAspLeuAsnPheLeuGlyIyGlyPhe 97
DB 517975 AAGGCTGTTTTCCTGCACTACGGAATCT-----TTAAGCTTTCGCGTAAGGCTAC 517922
QY 98 SerPheThrPheSerAsnIleAspAlaThrAlaSerGlyAlaIalIleGlySerGlu 117

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Db 517921 TCACCTTCTTTTAAAT---ATNAGTCTAGTGTGAAAGGCGCANA-CTT---TCTGTT 517869
 Qy 118 AAlaalaenlythrValThrleuserglYpHeserAlaleuserPheleuysSerPro 137
 Db 517868 ACACCTGATTAATAAATCTGTCCTTAACAGGATTTTGAGTCTTACTTTCTTACGGGCCCA 517809
 Qy 138 AAlaserthrValThr----- 142
 Db 517808 TCATCGGTAATCAACAACCCCTCAGAGAAAGGTGAGTAAATGTGAGGGGATCTTACA 517749
 Qy 143 -----AenGly-Leu----- 145
 Db 517748 TTTGATTAACAATGAACTATTATTATTAACAAGATTACTGTGAGGAAATGCGGACAT 517689
 Qy 145 ----- 145
 Db 517688 TTCTACAGAAATCTTTCTTTGAAAAACGACGCGGATGATTTCTTTGAAAGGAATTA 517629
 Qy 145 ----- 145
 Db 517628 ATCGAGCGCAACAGGAAAAAGGTGGGCTATTGTGCTACTGTAAGTATTAATTC 517569
 Qy 146 -----GlyValAl1 148
 Db 517568 AATATAACGGCTCTACCTCTCTCGAACATATATTCGAGAGCTGACGTGAGCTAT 517509
 Qy 148 eAnvalyVsglyAenleuserleuAenAenAenlyVsal1leuAenleuAenAenAen 168
 Db 517508 AATATGACAGAAATCTGTAACATTAACAGGAATGCTCTCTGTTATTTTCTGAAATATG 517449
 Qy 168 eSerThr-----GlyAenPglYglYAla1leuAenCyAla1leuAenleuAenleu 185
 Db 517448 TGTGACAGGACCGGAGAAATGAGAGACTCTTCTGAGANTGCGAGTATACATATTC 517389
 Qy 185 aAenAenlyVserleuserPhe1leuAenSerSerThrAenGlyVglYAla1leu 205
 Db 517388 TCGGATCTTACAGATGTAATCTTCTCAGAGAAACCAACCTGTAAGTATGCGGAGCCATTTA 517329
 Qy 205 eThrlyAenleuThrleuserSer-----GlyGlyluThrlAenPhe-GlnGlyA 222
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 Qy 222 eThrlyAenProThrAla1leuAenlyVsglyVglYAla1leuAenleuAenleu 242
 Db 517268 TATGCAAGGTATACACTGACAGTAATGTGAGGACATTTCTATCTGAGCGAGGAGAT 517209
 Qy 242 euserleuserglYpHeserGlyAenPhe1leuAenleuAenleuAenleuAenleu 261
 Db 517208 GTAGCTTCTCAGACAGAGGAGGACATTAACCTCAATGGAATGCCATTTGTGCAACTA 517149
 Qy 262 -----GlyThrValSerHiserAla1leuAenleuGlyThrSerAla1leuAenleu 280
 Db 517148 CACCAACAACTACGAAAGAAATATCTATGACATGATCTACTGCAAAAGATCACAATT 517089
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 Db 517088 TACGAGCAATATCTGAGGATAGATCTTTTCTACATCCGATTAATCTGATTAACGCGC 517029
 Qy 300 hSerValAlaAenPhe1leuAenleuAenleuAenleuAenleuAenleuAenleuAenleu 320
 Db 517028 CGGATTTCTACATTAATCTCAATTAAGCTGATGATGATGATGATGATGATGATGATGAT 516969
 Qy 320 hGlyThrlyVsglyVsglyVsglyVsglyVsglyVsglyVsglyVsglyVsglyVsgly 340
 Db 516968 GTGGGTCGATGTTTCTGCGGAAAGGCTCTCTAAGATGAAAGGAAAGTTGACAGACA 516909
 Qy 340 aAenlyThrSerlyVsglyVsglyVsglyVsglyVsglyVsglyVsglyVsglyVsglyVsgly 360
 Db 516908 ACCTGACTCTTACGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 516849
 Qy 360 lYpHeserValleuserAlaenGlyPheSerGlnAenPhe1leuAenleuAenleuAenleu 380
 Db 516848 GTGGTCTCACTCTGATGAAAGGCTTATCTACAGACGCGGGTCTCTGTTATATATG 516789

Qy 380 sPleuGlyThrSerleuValAlaenThrGlnuserleuGluThrlAenleuGluAla 400
 Db 516788 ATGGGGGACACACCTTAACACAGATACAGAGGAGTCACTTAACAGATCTTTCATATTC 516729
 Qy 400 sNleAenSerleuAenGlnGlyVsglyVsglyVsglyVsglyVsglyVsglyVsglyVsgly 420
 Db 516728 CTGTAAGCTCTTATAGGCGAGGAGTAAAGAAAGTGAATGCTGCTCTTCTCAGCAAGTAAAG 516669
 Qy 420 sPleAenlyVsglyVsglyVsglyVsglyVsglyVsglyVsglyVsglyVsglyVsgly 440
 Db 51668 ATGAGCCCTTATGAGTCTGAGATCTTCTTGTGATTAACAAAGGAGTCTTATGAAATTC 516609
 Qy 440 lYpHeserValleuserThrAenGlyVsglyVsglyVsglyVsglyVsglyVsglyVsgly 460
 Db 516608 ACAGACTAGAAAAACCAACATTT---TCATTTGTGACACTCTGCT---CTGGGTA 516555
 Qy 460 lValleuserAlaenPheSerAenGlnuserleuAenPhe1leuAenleuAenleuAenleu 478
 Db 516554 CTGCAACAACTACAGATGCTCCAGCGGTTCTTACAGTGAACATCTTACGCACTATGGGT 516495
 Qy 478 lYpGlnGlyVsglyVsglyVsglyVsglyVsglyVsglyVsglyVsglyVsglyVsgly 492
 Db 516494 ATCAAGGTACTTGGGAAATGACTTGGGTTGATGATACCCGACGACCTCCAAAGACTAAGA 516435
 Qy 492 lYpAenThrValSerThrAla1leuAenleuAenleuAenleuAenleuAenleuAenleuAenleu 512
 Db 516434 CAGGACATTTAGCTTGGACCAATACGGGCTACCTTCCGAATCTGAGGCTCAAGGACCTT 516375
 Qy 512 eUvalProAenleuThrPglYserPhe1leuAenPhe1leuAenPhe1leuAenPhe1leu 532
 Db 516374 TAGTCTTAATAGCTTGGGATCTTTTTCAGATCAATCAACGATTCAGGCTGATCAG 516315
 Qy 532 lYpGlnGlyVsglyVsglyVsglyVsglyVsglyVsglyVsglyVsglyVsglyVsgly 552
 Db 516314 AGAGAGGCTTGTGACTTGTTCAGATCAAGGCTTGTGGCTGGGAGCGCAAT 516255
 Qy 552 aLleuHleuAenSerGlyAenGlnAenGlnAenGlnAenGlnAenGlnAenGlnAenGlnAen 572
 Db 516254 TCTTATGATTAAGATTAAGAAAGGAGGAAACCAATACCGTATTAATCTGATGATATG 516195
 Qy 572 aLvalGlyAenSerThrAenPhe1leuAenPhe1leuAenPhe1leuAenPhe1leu 592
 Db 516194 CTATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 516135
 Qy 592 eUphAlaAenPhe1leuAenPhe1leuAenPhe1leuAenPhe1leuAenPhe1leuAenPhe1leu 612
 Db 516134 TCTTGTGATGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 516075
 Qy 612 eLleuAenGlnGlnHleuAenPhe1leuAenPhe1leuAenPhe1leuAenPhe1leuAenPhe1leu 632
 Db 516074 CCTTATATATCAACACATTAACAGATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 516016
 Qy 632 lYpGlyAenGlnGlnHleuAenPhe1leuAenPhe1leuAenPhe1leuAenPhe1leuAenPhe1leu 652
 Db 516015 -----CTTCTGCTGCTTGGAGTCAATTAACCTCTGTTTGAAG 515976
 Qy 652 lYpGlnleuserThrGlyHisThrAenPhe1leuAenPhe1leuAenPhe1leuAenPhe1leuAenPhe1leu 672
 Db 515975 GCGACCTGCTTATAGCAGCAGTCAATTAAGATTAAGATTAAGATTAAGATTAAGATTAAGATTA 515916
 Qy 672 rOProThrleuserThrAenPhe1leuAenPhe1leuAenPhe1leuAenPhe1leuAenPhe1leu 692
 Db 515915 AGGTG-----AAAGTCTTGGGGAATTAAGCTTTTAACATGATGTTGG 515871
 Qy 692 lYpThrAenValAlaValAenThrSerGlyAenGlyPhe-----P 706
 Db 515870 GA-----GCTTCTCTCATCTTATCTGATTAACCTGATGATTT 515832
 Qy 706 hGln 726
 Db 515831 TTGATTAACCTATGCTCATATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 515772

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Qy 726 aGluLeuGlyValAlIeSerAqPheSerApsSerHisLeuTYrAnIleValIleP 746
Db 515771 CGGAGAAAGCTACAGAGAGAGATCTTTGAGACAGCAACCTTCATTATCTTGC 515712
Qy 746 ToleuGlyIleLeuLeuGlyIuYrAqPheAla-----GluInTYrYrHisValY 763
Db 515711 CTATATGGGGTGAAGTTTGAAG---TTCTGATGTATATGACTTTTCTTATGATCTGA 515655
Qy 763 aAlaMetYrSerProApsValCYsAqSerApsProLYsCYsThrThrIleuLeuS 783
Db 515654 CTTATATCTTATGTTCTCTATCTTATCCGGAATGATCCAAATGCACTTACGACCTGTAA 515595
Qy 783 eArAnGInGlySerTrpLYsThrLYsGlySerApsLeuAlaArgGInAlaGlyIleValG 803
Db 515594 TCAGCGAGACCTCTTGGGAAACTTATGCAATTAATCTTACACAGACGCTTGCAAGTGC 515535
Qy 803 InAlaSerGlyPheArqSerLeuGlyAlaAlaGluLeuPheGlyApsPheG 823
Db 515534 GTGACGGACGATCATCACTACGCTTCTCTCTATGTTTGAATGATGCTCGGCGAGTTGTCTTTG 515475
Qy 823 InTPArqGlySerSerAqPheSerTYrAnValApsAlaGlySerLYsIleLYsPhe 841
Db 515474 AAGTTCTGATCTCTACGAGATTTATATGATGATCTTGGGGGTAAATTCATATTC 515419

RESULT 3
US-09-556-877-182
/ Sequence 182, Application US/09556877
/ Patent No. 6432916
GENERAL INFORMATION:
/ APPLICANT: Probst, Peter
/ APPLICANT: Bhatia, Ajay
/ APPLICANT: Skeiky, Yasir
/ APPLICANT: Fling, Steve
/ APPLICANT: Maisonneuve, Jeff
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
/ TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
/ FILE REFERENCE: 210121.469C5
/ CURRENT APPLICATION NUMBER: US/09/556,877
/ CURRENT FILING DATE: 2000-04-19
/ NUMBER OF SEQ ID NOS: 305
/ SOFTWARE: PaSeq for Windows Version 3.0/4.0
/ SEQ ID NO 182
/ LENGTH: 3021
/ TYPE: DNA
/ ORGANISM: Chlamydia
US-09-556-877-182

Alignment Scores:
Pred. No.: 5,22e-91 Length: 3021
Score: 939.00 Matches: 285
Percent Similarity: 39.77% Conservative: 127
Best Local Similarity: 27.51% Mismatches: 334
Query Match: 21.86% Indels: 290
DB: 4 Gaps: 29

US-09-830-446-27 (1-841) x US-09-556-877-182 (1-3021)
Qy 36 PheApsGlyThrThrSerThrThrSerPheSerSerLYsThrSerSerAlaThrApsGly 55
Db 91 TACATGCGAGACCTTAACTATCACTTCCCTTATCACTGTTATAGAGATCCGAGTGG 150
Qy 56 ThrAnTYrValPheLYsApsSerValValIleGluApsValProLYsThrGlyInThr 75
Db 151 ACTACTGTTTTCGACAGAGAGATTAACTTAAAAAATCTTGAACAATCTATTCAGACT 210
Qy 76 GlnSerThrSerCYsPheLYsApsAnPheAlaAlaGlyApsLeuApsPheLeuGly 95
Db 211 TTGCTTAAAGTTGTTTGGGAAAC-----TTATTAAGGAGTTTAACTGTTTAAAGGAGA 264
Qy 96 GlyPheSerPheThrPheSerAnIleApsAlaThrThrAlaSerGlyAlaAlaIleGly 115
Db 265 GGACACTCGTTGACTTTGAGAAACATA---CGACTTTCACAAATGGGGGAGCTTAAGT 321

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Qy	116	SerGIuIaIaAaenLyThrValThreusSerGIyPheSerAlIeuserPhe-----	133
Db	322	AAATGCGCTGCTGATGAGCTGTTACTTACTTGAAGGTTTTAAAGATTATCTTTCCAT	381
Qy	134	-----LeuysSerPro	137
Db	382	TGCAATTCACTTACCTGCCGTACTGCCCTGCGCAAGCACTAATAAAGGATGCCAGACTCCG	441
Qy	138	AlAserThrValThrAengLyLeuGIyAlaIleAenValLyPGLyAsnLeuSerLeuLeu	157
Db	442	ACGCAACATCTTACACCGCTCTAATGGTCTATTATTTCTTAAACAGATCTTTTGTATAC	501
Qy	158	AspAsnApLySerValLeuIleGLIAspAsnPheSerThrGIyAspGIyGIyAlaIleAen	177
Db	502	AATATATGAAAGTTCTCATTTCTATATGATATTTAGTCTCTGGAGATGGGGAGCTATAGAT	561
Qy	178	CysAlaGIySerLeuLySile-----	184
Db	562	---GCTAAGACCTTACGCGTTCAAGGATTTAGCAAGCTTTGTGTCTTCCAGAAATACT	618
Qy	185	-----AlaAsnAen	187
Db	619	GCTCAAGCTGATGGGGAGCTTGTTCAGATGACACAGTTTCTCTATGCTATGCTAAGCGAG	678
Qy	188	LySerLeuSerPheIleGIyAsnSerSerSerThrArgGIyGIyAlaIleHisThr---	206
Db	679	GCTCTATGTGCTTTGTATGCGAATGTTGACAGAGTAAAGGGGGAGGATTCGTCTGTT	738
Qy	206	-----	206
Db	739	CAGATGGGCGACGAGAGTGCATCATCTACTTCAACAGAAATCCAGTACTAGTTT	798
Qy	206	-----	206
Db	799	TCCAGAAATACGCGGTAGAGTTTGATGGGAACGTAGCCCGAGTAGAGAGGATTTAC	858
Qy	207	-----LyAsnLeuThrLeuSerSerGIyGIuThrLeuPheGLIyAsnThrAla	224
Db	859	TCCTACGGGACGTTGCTTCTTCTCGAATATATGAAAAACCTTGTCTTCAACAATGTGCT	918
Qy	225	-----ProThr	226
Db	919	TCTCTGTTTACATTTGCTGCTAAGCAACCAACAGTGGACAGGCTTTCTAATACGTAAT	978
Qy	226	-----	226
Db	979	AATTAACGAGATGAGAGGACTATCTTCTGTAAATGTGCGCAAGCAGATCCAATAAC	103
Qy	227	-----AlaAla	228
Db	1039	TCTGGATCAGTTTCTTTGATGAGAGGAGATGTTTCTTTAGTAGCAATGTAGCTGCT	109
Qy	229	GIyLyS-----	230
Db	1099	GGGAAAGGGGAGCTATTATGCCAAAAAGCTCTCGGTTGCTTAACTGTGCGCTGTACAA	115
Qy	231	-----GIyGIyAlaIleAlaIleAlaAspSerGIyThrLeu	242
Db	1159	TTTTTAAGGAATATCGCTAATAGATGTGTGAGGATTTATTTAGAGAACTGTGAGAGCTC	121
Qy	243	SerIleSerGIyAspSerGIyAspIleIlePheGLIy-----	255
Db	1219	AGTTTATCTGCTGATTTATGAGATATATTTTTCATGTGGAAATCTTAAAGAAACAGCCAAA	127
Qy	256	---AsnThrIleGIyAlaThrGIy---ThrValSerHisSerAlaIleAspLeuGIyThr	273
Db	1279	GAGAAATGCTCCGATGTTAATGGCGTAACTGTGTCTTCAACAAGCAATTTCCATGGATGG	133
Qy	274	SerAlaLySileThrAlaLeuArgAlaIleAGIyHisThrIleTyPheTyAspPro	293
Db	1339	GGAAGGAAAAATACAGACATTAAGAGCTTAAAGAGGCAATCAGATTCTCTTAATATGATCC	139
Qy	294	IleThrVal---ThrGIySerThrSerValAlaAspAla-----LeuAsnIleAen	309

Db 1399 ATCGAAGTGGCAACGAAATATACCGACCGACGCGCTTCCAAATCTCTAAAAATTAAC 1458
 QY 310 SerProAspThrGlyIaepAsnLysgluYrThrGlyThrIleValPheSerGlyLys 329
 Db 1459 -----GATGCTGAAGGAATACACAGGGCATATGTTTTTGC----- 1494
 QY 330 LeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSerLysLeuGlnAsnVal 349
 Db 1495 -----AATGGAAGCACTACTTGTCACAAATGCT 1524
 QY 350 AlaPheLysAsnGlyThrValValLeuLysGlyLysPheValValLeuSerAlaAsnGlyPhe 369
 Db 1525 ACGATAGACGACGAAGAGATGTTCTTCGTAAAAAGCAAAATTAATCATCGAATTCCTTA 1584
 QY 370 SerGlnAspAlaAsnSerLysLeuLleuLeuSerLeu----- 385
 Db 1585 AGTCAGACAGCTGGGAGT-----CTGTATATGGAAGCTGGGAATCACTTGATTTGTAACT 1641
 QY 386 -----ValAlaAsnThrGluSerIleGluLeuThrAsnLysGlu 398
 Db 1642 CCACACACCAACCAACAGCTCTCGCCGCTAATCATGTTATCAGCTTCCAACTCGCAT 1701
 QY 399 IleAsnLleAspSerLeuArgAsnGlyLysLysIle----- 410
 Db 1702 TTGCTCTCTTCTCTTGTGTAGCAAAACAATGCAATGCAAAATCCTCTCAACATCTCCA 1761
 QY 411 -----LysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAsp 424
 Db 1762 GCGCAAGATTCATCCTCGCAGCTATCTGTAGCACHACTGCTGTTCTGTTCATTAATAGT 1821
 QY 425 ArgProValValLeuAlaIleSerAspLysSerPheYrGlnAsnGlyPheLeuAsnGlu 444
 Db 1822 GGGCTATCTTTTGTGAAGATTGGATGATATACGCTTATGATAG----- 1866
 QY 445 AspiHisSerTyrAsp-----GlyIleLeuGlnLeuAspAla 456
 Db 1867 -----TATGATGGCTAGGTTCTAATCAAAAAATCAATGCTCTGAATTCACAGTTA 1917
 QY 457 GlyLysAspIleValIleSerAlaAspSerArgSerIleAspAlaValAlaGlnSerPro--- 475
 Db 1918 GGGACTAAGCCCCCAAGTATGCCCCCATCAAGTTGACTCTAGGAAATGAAGATGCCATAAG 1977
 QY 476 TyrGlyYrGlnGlyLysTyrThrIleAsnTyrSerThrAspAspLys----- 491
 Db 1978 TATGGCTATCAAGGAAGCTGGAAGCTTGCAGGATCTTAATACAGCAAAATATAGTCTCT 2037
 QY 492 -----LysAlaThrValSerTyrPheLysGlnSerPheAsnProThrAlaGln 508
 Db 2038 TATACTCTGAAGCTACA-----TGGACTAAACCTGGGTATTAATCCCGGCTCGAGCGA 2091
 QY 509 GluAlaProLeuValProAsnLeuLeuTyrGlySerPheIleAspValArgSerPheGln 528
 Db 2092 GTAGCTTCTTGGTTCGAAATAGTTTATGGGGATCATTTTATGATATACATCGCGCAT 2151
 QY 529 AsnPheIleGluLeuGlyThrGluGlyValaProYrGlyLysArgPheTyrValaGly 548
 Db 2152 TCAGCAATTCAGCAAGTGGATGGGGCTCTTATGTCCAGAGATTATGGGTTTTCGGA 2211
 QY 549 IleSerAsnValLeuHisArgSerGlyArgGluAsnGlnArgLysPheArgHisValSer 568
 Db 2212 GTTTCGAATTTCTTCTATCATGACCGCATGCTTAAAGCTGAAGGATATCGGATATTTAGT 2277
 QY 569 GlyGlyAlaValaGlyAlaSerThrArgMetProGlyGlyAspThrLeuSerLeuGly 588
 Db 2272 GGGGTTATCTCTTAGAGCAACTCTTACTTT---GATATCATGATGTTGGTCTTACGA 2328
 QY 589 PheAlaGlnLeuPheAlaArgAspLysAspYrPheMetAsnThrAsnPheAlaLysThr 608
 Db 2329 TTATCCGAAGATATTGTTAGATCTAAAGATTATGATGATGTCGTTCAAATCATCATGCT 2388
 QY 609 TyrAlaGlySerLeuArgLeuGlnHisAspAlaSerLeuYrSerValValSerIleLeu 628

Dd	2389	TGCAATGAGATCCGTTATTCATCTACCAACAAGCTTAACTGGA-----TCTATATTG	2442
Qy	629	LeuGlyGluGlyLeuAlaGlyGluIleLeuLeuProTyrValSerLysThrLeuProCys	648
Dd	2443	TTCCGAGATCGCTTTATCCCT-----	2463
Qy	649	SerPheTyrGlyGlnLeuSerTyrGlyHisThrAspHisArgMetLysThrGlnSerLeu	668
Dd	2464	-----GCTAGCTACGGGTTTGGGAAATACGATGAAACCTCATAT---	2505
Qy	669	ProProProProProThrLeuSerThrAsp---HisThrSerTyrGlyTyrValTyr	687
Dd	2506	-----ACATTTCAGAGAGAGGCGATGTGTTGGGAAATAACTGCTCG	2550
Qy	688	AlaGlyGlnLeuGlyThrArgValAlaValGlnAsnThrSerGlyArgGlyPhePheGln	707
Dd	2551	GCTGGAAAGATTTGAGGGGATTAACCATGTGATTAATCATCATTAAGCTCTATTGAAT	2610
Qy	708	GlnTyrThrProPheValLysValGlnAlaValTyrAlaArgGlnAspSerPheValGlu	727
Dd	2611	GAGTTGGCTCTTTTCGTCGAAGCTGAAGTTTCTTATGCCATCATGAATCTTTTACGAG	2670
Qy	728	LeuGlyAlaIleSerArgAspPheSerAspSerHisLeuTyrAsnLeuAlaIleProLeu	747
Dd	2671	GAAGGCGATCAAGCTCGGCGCATTCAAAGCGGACATCTCTAAATCTATCAGTTCCTGT	2730
Qy	748	GlyIleLysLeuGlyLysArgPheAla-----GlnGlnTyrTyrHisValAlaIleMet	765
Dd	2731	GGATGTGAAGTTTATGTCGATGTCTTAGTACACATCTTAATAATTAAGCTTTATGGCGCT	2790
Qy	766	TySerProAspValCysArgSerAsnProLysCysThrThrThrLeuLeuSerAsnGln	785
Dd	2791	TATATCTGTATGTTATCCGACACATCTCTGTAAGTGAACAAGCTCTTATCCCATCA	2850
Qy	786	GlySerTyrLysThrLysGlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSer	805
Dd	2851	GAGCATGAGCAACAGATGCCCTTCATTTAGCAAGACATGAGTTGTGTAGAGGATCT	2910
Qy	806	GlyPheArgSerLeuGlyAlaAlaAlaGlnLeuPheGlyAsnPheGlyPheGlnTyrArg	825
Dd	2911	ATGTATCTCTCTCAACAGATTAATTAAGTAAATATATGATGATGCGCATGGAAGATTAAGATTCGA	2970
Qy	826	GlySerSerArgSerTyrAsnValAspAlaGlySerLysIleLysPhe	841
Dd	2971	GATGCTTCTGAGGCTATGTGTTTAGTCGACGAAGTAAAGTCCGCTTC	3018
RESULT 4			
	US-09-620-412C-182		
	: Sequence 182, Application US/09620412C		
	: Patent No. 6448234		
	: GENERAL INFORMATION:		
	: APPLICANT: Steven P. Fling		
	: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND		
	: FILE REFERENCE: 210121.469C7		
	: CURRENT APPLICATION NUMBER: US/09/620,412C		
	: CURRENT FILING DATE: 2000-07-20		
	: NUMBER OF SEQ ID NOS: 363		
	: SOFTWARE: FastSeq for Windows Version 3.0/4.0		
	: SEQ ID NO 182		
	: LENGTH: 3021		
	: TYPE: DNA		
	: ORGANISM: Chlamydia		
	US-09-620-412C-182		
Alignment Scores:			
	Pred. NO.:	5.22e-91	3021
	Score:	939.00	285
	Percent Similarity:	39.77%	127
	Best Local Similarity:	27.51%	334
	Query Match:	21.86%	290
	DB:	4	Gaps: 29


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QY 529 AenPheIleuGluThrGluValAlaProTyrGluValArgPheTrpValaGly 548
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DB 2152 TCAGCAATTCAGCAAGATGGATGGGCTTATTCGACGATTATGGCTTCGA 2211
QY 549 ILeSerAenValLeuHleArgSerGlyArgGluAenGlnArgPheArgHleValSer 568
   ::::::::::::::::::::
DB 2212 GTTTCGAATTCCTTCATCAAGACCGCATGCTTATAGGTGAGGATATCGGATATTAAGT 2271
QY 569 GIVGIVAlaValAlaGIVAlaSerThrArgMetProGIVGIVAlaPheThrLeuSerIleu 588
   ::::::::::::::::::::
DB 2272 GGGGGTATTCCTTACGAGCAAACTCTTACTT---GATTCATCGATGTTGGCTTACGA 2328
QY 589 PheAlaGlnLeuPheAlaArgAspLysAspTyrPheMetAenThrAenPheAlaLysThr 608
   ::::::::::::::::::::
DB 2329 TTTACCGAAGATATTGGTAAATCTTAAGATTATAGAGTGTGCTTCACATCATATGCT 2388
QY 609 TyrAlaGlySerLeuArgLeuGlnHleAspAlaSerLeuTyrSerValValSerIleu 628
   ::::::::::::::::::::
DB 2389 TGCATAGCATCCGTTATCTATCTATCCCAACAAAGCTTATATGGA-----TCCATATTG 2442
QY 629 LeuGIVGIVGIVGIVLeuArgGluIleLeuLeuProTyrValSerLysThrLeuProCys 648
   ::::::::::::::::::::
DB 2443 TTCGAGAAATGGCTTATCCGT----- 2463
QY 649 SerPheTyrGIVGIVLeuSerTyrGIVHleThrAspHleArgMetLysThrGluSerLeu 668
   ::::::::::::::::::::
DB 2464 -----GCTAGCTACGGGTTTGGGAATTCAGCATATGAAAACCTCATAT--- 2505
QY 669 ProProProProProThrLeuSerThrAsp--HleThrSerTyrGIVGIVTyrValTrp 687
   ::::::::::::::::::::
DB 2506 -----ACATTCGACAGAGAGAGCGATGTTGCTGGGATTAATTAACGTCTG 2550
QY 688 AlaGIVGIVLeuGIVTyrArgValAlaValAlaGluAenThrSerGlyArgGIVPheHleGln 707
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DB 2551 GCTGAGAGATATTGAGCGGATTCACCATGTCATTCATCCATTAAGCTCATATTGAAT 2610
QY 708 GIVTyrThrProPheValLysValGlnAlaValTyrAlaArgGlnAspSerPheValGlu 727
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DB 2611 GAGTTGCGCTCTTTCGTGACAGCTGATTTCTTATGCGCATCAAGATCTTTTACAGAG 2670
QY 728 LeuGIVAlaIleSerArgAspPheSerAspSerHleuTyrAenLeuAlaIleProLeu 747
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DB 2671 GAAGCGCATCAAGCTCGGCGCATTCAGAGCGGACATCTCTTAATCTATCAAGTCTCTGT 2730
QY 748 GIVLysLysLeuGlnLysArgPheAla-----GluGlnTyrTyrHleValValAlaMet 765
   ::::::::::::::::::::
DB 2731 GAGTGAAGTTCATGATCGATGTTCTAGTACATCTCAATTAATTAATAGCTTATAGCGGCT 2790
QY 766 TyrSerProAspValCysArgSerAenProLysCysThrThrThrLeuLeuSerAenGln 785
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DB 2791 TATATCTGATGATCTTATTCGACATCTCTGATCTGACAGACAAACGCTCTTATCCATCA 2850
QY 786 GIVSerTrpLysThrLysLysSerAenLeuAlaArgGlnAlaGlyLysValGlnAlaSer 805
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DB 2851 GAGACATGAGCAACAGATGCTTTCATTTAGCAAGACATGAGAGTGTGATTAGAGATCT 2910
QY 806 GlyPheArgSerLeuGIVAlaAlaAlaGIVLeuPheGlyAenPheGlyPheGIVTrpArg 825
   ::::::::::::::::::::
DB 2911 ATGATGCTTCTCTTAACAGATATAGAAAGTATAGGCGCATGAAGAAATAGATATGCA 2970
QY 826 GIVSerSerArgSerTyrAenValAlaPheAlaGIVSerLysLysLysPhe 841
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DB 2971 GATGCTTTCGAGGCTATGCTTATGATGAGAGAAATAGATCGGCTTC 3018

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RESULT 5

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US-09-598-419-182
; Sequence 182, Application US/09598419
; Patent No. 6565856
; GENERAL INFORMATION:
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Scholler, John
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

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; FILE REFERENCE: 210121.469C6
; CURRENT APPLICATION NUMBER: US/09/598, 419
; CURRENT FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 357
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 182
; LENGTH: 3021
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-598-419-182

Alignment Scores:
Pred. No.: 5,22e-91 Length: 3021
Score: 939.00 Matches: 285
Percent Similarity: 39.77% Conservatave: 127
Best Local Similarity: 27.51% Mismatches: 334
Query Match: 21.86% Indels: 290
DB: 4 Gaps: 29

US-09-830-446-27 (1-841) x US-09-598-419-182 (1-3021)

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DB 91 TACGATGGGAGAGAGATTAACTGATCATTTCTCTATACCTGTTATAGAGATCCAGTGG 150
QY 56 ThrAenTyrValPheLysAspSerValValIleGluAenValProLysThrGIVLysThr 75
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DB 151 ACTACTGTTTTTTCGACGAGAGATTAACATTAATAAAATCTTGACAAATTCATATTCGACT 210
QY 76 GIVSerThrSerCysPheLysAenAspAlaAlaAlaGIVAspLeuAenPheLeuGIVLys 95
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DB 211 TTGCTTTATATGTTTGGGAACT-----TTATTAGGAGAGTATTACGTTTATAGGAGA 264
QY 96 GIVPheSerPheThrPheSerAenIleAspAlaThrThrAlaSerGIVAlaAlaIleGly 115
   ::::::::::::::::::::
DB 265 GAGACATCTGTTGACTTCGAGAACATA---CGACTCTTACAAATGGGCGACTTAAGT 321
QY 116 SerGIVAlaAlaAenLysThrValThrLeuSerGIVPheSerAlaLeuSerPhe----- 133
   ::::::::::::::::::::
DB 322 AATAGCGCTGCTGATGAGCTGTTTACTATTAAGAGGTTTAAAGATTAATCTTTTCCAAAT 381
QY 134 -----LeuLysSerPro 137
   ::::::::::::::::::::
DB 382 TGCAATTCATTAATTCGCGTACTGCTGCTGCTGCAACGATTAATAGGTAAGCCAGCTCG 441
QY 138 AlaSerThrValThrAenGIVLeuGIVAlaIleAenValLysGIVAsnLeuSerLeu 157
   ::::::::::::::::::::
DB 442 ACGACATCTTACACCGCTTAATGTAATTAATCTTAATAACAGATCTTTGTTACTC 501
QY 158 AspAenAspLysValLeuIleGlnAspAenPheSerThrGIVAspGIVGIVAlaIleAen 177
   ::::::::::::::::::::
DB 502 AATATATGAAAGTCTCTATTTATATGTAATTAATTAATTAATTAATTAATTAATTAAT 561
QY 178 CysAlaGIVSerLeuLysIle-----AlaAsnAen 184
   ::::::::::::::::::::
DB 562 ---GCTAAGACTTAACGCTTCAAGAAATTAGCAAGTTTGTCTTCCAGAAAATACT 618
QY 185 ----- 187
   ::::::::::::::::::::
DB 619 GCTCAAGCTGATGGGAGCTTGTCAAGTACTCAACAGTTTCTGCTAAGGCTTAACAG 678
QY 188 LysSerLeuSerPheIleGIVAsnSerSerThrArgGIVGIVAlaIleHleThr--- 206
   ::::::::::::::::::::
DB 679 GCTCTATATGCTTGTATGCAATGTTTCCAGAGATAGAGGGAGGATGCTGCTGTT 738
QY 206 ----- 206
   ::::::::::::::::::::
DB 739 CAGATGGGAGAGAGGTGTCATCATCTTCAACAGAAATCCAGTAGTAATTTT 798
QY 206 ----- 206
   ::::::::::::::::::::
DB 799 TCAGAAATTAATCTGCGGTAGAGTGTGATGCGGAACGTAGCCGAGTAGAGAGGATTTAC 858

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QY 207 -----LysAsnLeuThrIleuSerSerGlyGlyIuThrIleuPheGlnGlyAsnThrAla 224
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 DB 859 TCCTACGGGAAAGCTGTCTTCTGTAATATATGAAAAACCTGTTCTCAACAATGTTGCT 918
 QY 225 -----ProThr----- 226
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 DB 919 TCTCTGTTTACATTCCTGTAACCAACCAAGTGAAGAGCTTCTATACAGTAAT 978
 QY 226 ----- 226
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 DB 979 AATTACGAGATGAGAGAGCTATCTTGTAAATGTCGCAAGAGATCCAAATAC 1038
 QY 227 -----AlaAla 228
 |||:::|
 DB 1039 TCTGATCAGTTTCTTGTATGAGAGAGAGTGTCTTTAGTAGCAATGAGCTGCT 1098
 QY 229 GlyLys----- 230
 |||:::|
 DB 1099 GGGAAAGGGGAGCTATTATGCAAAAGCTCTCGTTGCTAATCTGGCCCTGTACAA 1158
 QY 231 -----GlyGlyAlaIleAlaIleAlaIleAspSerGlyThrIleu 242
 |||:::|
 DB 1159 TTTTAAAGAAATATCGCTAATGATGTGAGAGCAATTTATAGAGAAATCTGAGAGCTC 1218
 QY 243 SerIleSerGlyAspSerGlyAspIleIlePheGlnGly----- 255
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 DB 1219 AGTTTATCTGCTGATTAATGAGATATTTATTTGATGGAATCTTAAAGAACAGCCAA 1278
 QY 256 ---AsnThrIleGlyAlaThrGly-----ThrValSerHisSerAlaIleAspLeuGlyThr 273
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 DB 1279 GAGAAATGCTGCCAGATGTAATGCGTAACTGTCTCCACAAAGCAATTCGATGGAGATCG 1338
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 DB 1339 GAGGAGAAATTAACGATTAAGCATTAAGCATTAAGCGGATCATGATTCCTTAAATGATCC 1398
 QY 294 IleThrVal---ThrGlySerThrSerValAlaAspAla-----LeuAsnIleAsn 309
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 QY 310 SerProAspThrGlyAspAsnLysGlyTyThrGlyThrIleValPheSerGlyGlyLys 329
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 QY 330 LeuThrGluAlaGluAlaLysAspGlyLysAspArgThrSerLysLeuGlnAsnVal 349
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 QY 370 SerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeu----- 385
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 QY 386 -----ValAlaAsnThrGluSerIleGluLeuThrAsnLeuGln 398
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 QY 399 IleAsnIleAspSerLeuArgAsnGlyLysLysIle----- 410
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 QY 411 -----LysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAsp 424
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 QY 425 ArgProValValLeuAlaIleSerAspGlySerPheTyroIleAsnGlyPheLeuAsnGly 444
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 QY 445 AspHisSerTyraPhe-----GlyIleLeuGluLeuAspAla 456

DB 1867 -----TATGATTTGGCTAGGTTCTAATCAAAAATCAATGCTCGAAATTAACAGTTA 1917
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 QY 476 TyroGlyTyroGlnGlyLysThrIleAsnThrPheSerThrAspAspLys----- 491
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 QY 492 -----LysAlaThrValSerThrAlaLysGlnSerPheAsnProThrAlaGlnGln 508
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 DB 2038 TATACTCTGAAGCTACA-----TCGACTAAACATGCGTATATCTCGGCTGAGAGCA 2091
 QY 509 GluAlaProLeuValProAsnLeuLeuThrGlySerPheIleAspValArgSerPheGln 528
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 DB 2212 GTTTCGAATTTCTTATCATGACCGCATGCTTTAGTCAGGAGATATCGGATATTAAT 2271
 QY 569 GlyGlyAlaValAlaGlyLysThrArgMetProGlyGlyAspThrLeuSerLeuGly 588
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 DB 2389 TGCATGAGATTCGGTATATCTATCTACCAACAAGCTTATGTCGA-----TCCATTTTG 2442
 QY 629 LeuGlyGlnGlyGlyLeuArgGluIleLeuLeuProTyroValSerLysThrLeuProCys 648
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 DB 2443 TTCGAGAGATGCGTTATTCCTT----- 2463
 QY 649 SerPheTyroGlyLysLeuSerTyroGlyHisThrAspHisArgMetLysThrGluSerLeu 668
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 DB 2464 -----GCTAGCTACGGGTTTGGAAATCAGCATATGAAACCTATAT--- 2505
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 QY 688 AlaGlyGlnLeuGlyThrArgValAlaValGluAsnThrSerGlyArgGlyPhePheGln 707
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 DB 2551 GCTGGAGATATGAGCGGAGATTAACGATGATTAATCTCAATCTAATCTAATCTAATCTAAT 2610
 QY 708 GluTyroThrProPheValLysValGlnAlaValTyroAlaArgGlnAspSerPheValGlu 727
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 DB 2611 GAGTTCGCTCTTCTGCGCAAGCTGATTTCTTATGCGGATGATGATGATGATGATGATGATGAT 2670
 QY 728 LeuGlyAlaIleSerArgAspPheSerAspSerHisLeuTyroAsnLeuAlaIleProLeu 747
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 DB 2671 GAAGCGATCAAGCTCGGCAATTCAGAGCGGACATCTCTAATCTAATCTAATCTAATCTAAT 2730
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 QY 766 TyroSerProAspValLysArgSerAsnProLysCysThrThrThrLeuLeuSerAsnGln 785
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 DB 2791 TATATCTGATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2850
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QY 370 SerGlnAspAlaSerIleu11eMeAspLeuGlyThreSerIleu----- 385
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QY 386 -----ValAlaAsnThrGluSerIleGluLeuThrAsnLeuGlu 398
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    1570 CCACAACACACACAGACGCTCTCGCGCTTAATCAGATTGATCAGCTTCCAACTGCGAT 1629
QY 399 IleAsnIleAspSerIleuArgAsnGlyLysIle----- 410
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QY 411 -----LysLeuSerAlaIleThrAlaGlnLysAspIleArgIleAsp 424
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QY 445 AspHisSerTyrlAsp-----GlyIleLeuGluLeuAspAla 456
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QY 457 GlyLysAspIleValIleSerAlaAspSerArgSerIleAspAlaValGlnSerPro--- 475
    |||||
    1846 GGGACATGAGCCCGACAGTATGCCCCATCAGATTGATGCTACAGGAATGAGATCCCTAAG 1905
QY 476 TyrlGlyTyrlGlnGlyLysTyrlThrIleAsnTyrlSerThrAspAspLys----- 491
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    1906 TATGGCTATCAGAGAGCTGGAAGCTTGGCGGATCTCAATACAGCAAAATTAATGCTCT 1965
QY 492 -----LysAlaThrValSerThrAlaLysGlnSerPheAsnProThrAlaGlnGlu 508
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    1966 TATACTCTGAAAGCTACA-----TGCACTAAACCTGGATATATCTGGGCTGAGCGCA 2019
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    2080 TCAGCAATTCAGCAAGTGTGATGGCGCTTATGTGAGAGATTAATGGTTCTCGCA 2139
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    2140 GTTTCGAAATTTCTTCTATCATGACCGCGATGCTTAGCTCAGGATATCGGTATATAGT 2199
QY 569 GlyGlyValAlaValGlyAlaSerThrArgMetProGlyLysAspThrLeuSerLeuGly 588
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    2200 GGGGCTTATCTTGAAGCAAACTCTACTTT---GATCATCATGATGTTGGCTAGCA 2256
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    2257 TTACCGCAAGTATTTGTAGATCTAAAGATTATAGTAGTGCTGCATCATCATGCT 2316
QY 609 TyrlAlaGlySerLeuArgLeuGlnHisAspAlaSerLeuTyrlSerValIleSerIleLeu 628
    |||||
    2317 TGCATAGGATCCGTTTATCTATCATCCCAACAGCTTAAATGTGA-----TCTATATTG 2370
QY 629 LeuGlyLysGluLysLeuArgGluIleLeuLeuProTyrlValSerLysThrLeuProCys 648
    |||||
    2371 TTGGAGATCGGTTTATCTCT----- 2391
QY 649 SerPheTyrlGlyLysLeuSerTyrlGlyLysIleThrAspHisValGserLysThrGluSerLeu 668
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    2392 -----GCTACCTAGCGGTTTGGGAATCAGCATATGAAACCTCATAT--- 2433
QY 669 ProProProProProThrLeuSerThrAsp---HisThrSerTyrlGlyLysTyrlValTyr 687
    |||||
    2434 -----ACATTTGCAAGAGAGAGAGATGTTGTTGGGATTAATACTGTCTG 2478

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QY 688 AlaGlyLysLeuGlyThrArgValAlaValGluAsnThrSerGlyArgGlyPhePheGln 707
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    2539 GAGTTCGCTCTTTCGTGCAAGCTGAGGTTTCTTAAGCCGATCATGATCTTTTACAGAG 2598
QY 728 LeuGlyValAlaIleSerArgAspPheSerAspSerHisLeuTyrlAsnLeuAlaIleProLeu 747
    |||||
    2599 GAAGCGATCAACCTCGGCACTTCAAGAGGACATCTCTTAATCTATACAGTCTCTGTT 2658
QY 748 GlyIleLysLeuGluLysArgPheAla-----GluGlnTyrlTyrlHisValAlaIleMet 765
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    2659 GAGGTGAAGTTGATGATGATGCTTCTAGTACATCATCTAATTAATATAGCTTATGCGGCT 2718
QY 766 TyrlSerProAspValCysArgSerAsnProLysCysThrThrThrLeuLeuSerAsnGln 785
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    2719 TATATCTGATGCTTATGCGACCATCTCTGTACTAGACAGACGCTCTATCCATCA 2778
QY 786 GlySerTyrlPheThrLysGlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSer 805
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    2779 GAGCATGACACACAGATGCTTCTTATGACAGACATGAGAGTGTGTTAAGCATCT 2838
QY 806 GlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTyrArg 825
    |||||
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QY 826 GlySerSerThrSerTyrlAsnValAspAlaGlySerLysIleLysPhe 841
    |||||
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QY 2899 GATGCTTCTGAGCTATGATGTTGAGTGCAAGGATGAATGATGCTGCTTCT 2946

RESULT 7
US-09-620-412C-170
; Sequence 170, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469CT
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 170
; LENGTH: 2949
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-170

Alignment Scores:
Pred. No.: 1.06e-90 Length: 2949
Score: 936.00 Matches: 285
Percent Similarity: 39.67% Conservative: 126
Best Local Similarity: 27.51% Mismatches: 335
Query Match: 21.79% Indels: 290
Gaps: 29

US-09-830-446-27 (1-841) x US-09-620-412C-170 (1-2949)
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Db 19 TACGATGGGAGAGAGCTTAATCTATATATTTCTTAACTGTTATAGAGATCCGAGTGGG 78
QY 56 ThrAsnTyrlValPheLysAspSerValIleGluAsnValProLysThrGlyGluThr 75
    |||||
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Db 79 ACTACGTTTTTCTGACAGAGATTAACATTAATAAAATCTATGACATCTATATGAGCT 138
QY 76 GlnSerThrSerCysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGly 95
    |||||
    139 TTGCTTTAAGTGTGTTGGAGC-----TTATTAAGGAGTTTATCTGTTTAAAGGAGA 192

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QY 96 glyPheSerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyValAlaIleGly 115
 DB 199 GGACACCTGGTACCTTGGAGAAACATA---CGACCTTCAACAATGGGACCTCAACT 249
 QY 116 SerGluAlaAlaAsnIleThrValThrIleuSerGlyPheSerAlaIleuSerPhe----- 133
 DB 250 AATTACGGCTGCTGATGAGACTGTTTACTATTGAGGGGTTTAAAGAAATTATCTTTTCCAAAT 309
 QY 134 -----LeuIleuSerPro 137
 DB 310 TCCAAATCACTTACCTGCGCTACTGCTGCTGCAACGACATAATAGGGTAGCCAGACTCCG 369
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 DB 370 ACGACAACTACACACCGCTAATGCTAATTTATCTTAAACAGATCTTTTGTACTC 429
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 QY 178 CyAlaGlySerLeuIleu----- 184
 DB 490 ---GCTAAGACTTAAACGCTTCAAGGAATTAGCAAGCTTGTGTCTTCCAGAAATACT 546
 QY 185 -----AlaAsnAsn 187
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 QY 188 LysSerLeuSerPheIleGlyAsnSerSerSerThrArgGlyValAlaIleIleThr--- 206
 DB 607 GCTCCATATGCTTGTGTAGCGAATGTGTGACAGAGTAGAGGGAGAGGAGTCTGCTGT 666
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 DB 667 CAGGATGGCAGACAGGAGTGTATCATCTTCAACAGAAAGTCAAGTACTGTAAGTTT 726
 QY 206 ----- 206
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 QY 207 -----LysAsnIleuThrIleuSerSerGlyGlyIleuThrIleuPheGlnGlyAsnThrAla 224
 DB 787 TCTTACGGGAACGTTGCTTCTGATTAATGGAAGAAACCTGTTTCTCAACATGTTGCT 846
 QY 225 -----ProThr----- 226
 DB 847 TCTCTGTTTACATGCTGCTAAGCAACAAAGTAGAGAGGCTTCTAATACAGATAAT 906
 QY 226 ----- 226
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 QY 227 -----AlaAla 228
 DB 967 TCTGATCAGTTTCTTGAATGAGAGAGAGTAGTTTCTTATAGTCAATGATAGCTGCT 1026
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 QY 231 -----GlyGlyAlaIleAlaIleAlaIleAspSerGlyThrIleu 242
 DB 1087 TTTTAAAGAAATATGCTAATATATGATGAGAGATTTATTTAGAGAAATCTGAGAGCTC 1146
 QY 243 SerIleSerGlyAspSerGlyAspIleIlePheGlnGly----- 255
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 QY 256 ---AsnThrIleGlyAlaThrGly---ThrValSerIleSerAlaIleAspLeuGlyThr 273
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 DB 1750 GGGCTATCTTTTGGAGATTTGATGATACAGTTATGATAG----- 1794
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 QY 476 TyrGlyTyrGlnGlyLysIleThrIleAsnIleAspIleAspAspLys----- 491
 DB 1906 TATGCTATCAAGAAAGCTGGAAGCTTCGTTGGAGTCTAATACAGCAATATAGTCTCT 1965
 QY 492 -----LysAlaThrValSerIleThrAlaLysGlnSerPheAsnProThrAlaGln 508
 DB 1966 TATACTGAAAGCTACA-----TGACTAAACCTGGATTAATCTGGGCTTACAGCA 2019
 QY 509 GluAlaProLeuValProAsnIleuLeuThrGlySerPheIleAspValArgSerPheGln 528
 DB 2020 GTAGCTTCTTGGCTCCAAATGATTTATGCGGATCATTTTAAATATAGATCTGCGCAT 2079
 QY 529 AsnPheIleGlyLeuGlyThrGlnGlyAlaProTyrGlyLysLysArgPheThrValAlaGly 548
 DB 2080 TCAGCAATTCAGCAAGAGTGGATGGGCGCTTATGTCGAGAGATTAATGGGTTCTGGA 2139
 QY 549 IleSerAsnValLeuHisArgSerGlyArgGlyAsnGlnAlaGlyLysPheArgHisValSer 568
 DB 2140 GTTTGAAATTTCTTATACATGACCGGATGCTTATAGCTACGGAGATATCGTAAATATGAT 2199
 QY 569 GlyGlyAlaValAlaGlyAlaSerThrArgMetProGlyGlyLysPheThrLeuSerLeuGly 588
 DB 2200 GGGGATTAATCTTGAAGCAAACTCTTAATTT---GATCATGCAATGTTTGTGTACGA 2256
 QY 589 PheAlaGlnLeuPheAlaArgAspLysAspTyrPheMetAsnThrAsnPheAlaLysThr 608

Db	2257	TTTACCGAAGATTGGTAGATCTAAAGATTATAGTAGTGTCGTCCAAATCAATCATGCT	2318
Qy	609	TyralaglySerLeuAagLeuGlnHlsAepAlaserLeuTyrservalValSerileu	628
Db	2317	TGCATAGGATCCGTTATCTATCTAACCACAAAGCTTATGTGA-----TCCATATTG	2370
Qy	629	LeuGlyGluGlyLeuAagGlnIleLeuLeuProTyrservalSerlysthLeuProCys	648
Db	2371	TTCCGAGATGCGTTATCCGT-----	2391
Qy	649	SerPheTyrcylGlnLeuSerTyrcylYHlsThrAphlsAsgmelysthGluSerLeu	668
Db	2392	-----GCTAGCTACCGGTTTGGGAATACGCAATGAAACCTCATAT---	2433
Qy	669	ProProProProProThrLeuSerThraP-----HlsThrSerTyrGlyTyrservalTyr	687
Db	2434	-----ACATTTGCAGAGAGACGCATGTCGTGGGATTAATACGTCTG	2478
Qy	688	AlaGlyGluLeuGlyThraGvalAlaValGlnbenthSerGlyAagGlyPhePheGln	707
Db	2479	GCTGAGAGATGTGAGCGGGAATTCACGATTCGATTAATCTCATCACTAATTTGAAT	2538
Qy	708	GluTyrThrProPheValysValGlnAlaValTyralaGlnAaspSerPheValGlu	727
Db	2539	GAGTTGCGCTCTTCGTCACAGCTGATTTCTTATTCGATCAATGAATCTTTTACAGAG	2598
Qy	728	LeuGlyAlaIleSerAraGaspPheSerAaspSerHlsLeuTyrsAenLeuAlaIleProleu	747
Db	2599	GAAAGCGCATCAAGCTCGGCGATTCGAAGCGGACATCTCCAAATCTATCGTCTCGTT	2658
Qy	748	GlyIleIleYsLeuGlnYsAraPheAla-----GluGlnTyrcylHlsValAlaIleMet	765
Db	2659	GGAATGAAGTTTGATCGATGTTCTACAGTACACATCTCAATTAATAGCTTATAGCGCGCT	2718
Qy	766	TyrsPProAapValCysAraSerAaspProlysCysThrThrThrLeuLeuSerAangln	785
Db	2719	TATATCTGATGCTTATTCGACCACTCTCGTACTAGACACAGCTCTATATCCATCAA	2778
Qy	786	GlySerTyrPylserThySgIySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSer	805
Db	2779	GAGACATGACAAACAGATGCCCTTCATCTTACCAAGACATGAGAGTGTGCTTAGAGCATCT	2838
Qy	806	GlyPheAraSerLeuGlyAlaAlaAlaGluLeuPheGlyAaenPheGlyPheGluTyrArg	825
Db	2839	ATGATATGCTTCTTCAACAGTAAATATAGAAATATATGCGCATGAGATAGATAGATCA	2898
Qy	826	GlySerSerAraGserTyrsAanValAapAlaGlySerlySleIleYsPhe	841
Db	2899	GATGCTTCTGAGGCTATGTTTGAATGTCAGAGATGAAGTCAATGCTTC	2946
RESULT 8			
US-09-598-419-170			
Sequence 170: Application US/09598419			
Patent No. 6565856			
GENERAL INFORMATION:			
APPLICANT: Skeiky, Yasir A.W.			
APPLICANT: Scholler, John			
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND			
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION			
FILE REFERENCE: 210121.469C6			
CURRENT APPLICATION NUMBER: US/09/598.419			
CURRENT FILING DATE: 2000-06-20			
NUMBER OF SEQ ID NOS: 357			
SOFTWARE: FastSeq for Windows Version 3.0/4.0			
SEQ ID NO 170			
LENGTH: 2949			
TYPE: DNA			
ORGANISM: Chlamydia			
US-09-598-419-170			
Alignment Scores:			
Pred. No.:		1.06e-90	Length: 2949
Score:		936.00	Matches: 285

Percent Similarity:	39.67%	Conservative:	126
Best Local Similarity:	27.51%	Mismatches:	358
Query Match:	21.79%	Indels:	250
DB:	4	Gaps:	29

QY	36	PhaAspG1ThrThrSerThrThrSerPheSerSerLeuThrSerSerAlaThrAspGly	55
Db	19	TACGATGGGAGACGTTAACTGATCAATTTCCCTTACTGTTATAGAGAGATCCGAGTGGG	78
QY	56	ThrAsnTyValPheIysAspSerValAlIleGluAsnValProIysThrGlyIuThr	75
Db	79	ACTACAGTTTTTTCTGCAGAGAGATTAACTAAATAAAATCTTGACAATTCATATTGCACT	138
QY	76	GlnSerThrSerCysPheIysAsnAspAlaAlaIleGlyAspLeuAsnPheLeuGlyGly	95
Db	139	TTGCCTTTAAGTGGTTTGGGAAC-----TTATTATGGAGCTTTTACTGTTTTATGGGAGA	192
QY	96	GlyPheSerPheThrPheSerAsnIleAspAlaThrTrpAlaSerGlyAlaAlaIleGly	115
Db	193	GGACACTCGTTGACTTTCAGAAACATA---CGAGCTTCAAAATGGGGCAGCTCTAGT	249
QY	116	SerGluAlaAlaAsnIysThrValThrLeuSerGlyPheSerAlaLeuSerPhe----	133
Db	250	AATATGGCTGTGATGAGCTGTTACTATTGAGGGCTTTAAAGAAATTATCTTTCCAAAT	309
QY	134	-----LeuIysSerPro	137
Db	310	TGCAAATTCATTACTGCCCTACTGCCCTGCTGCACAGCAATAATTAAGGTAGCCCAACTCCG	368
QY	138	AlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValIysGlyAsnLeuSerLeuLeu	157
Db	370	ACGACAACACTACACCCGCTAGTACTATTATCTTAATAACAGATCTTTGTCTACTC	429
QY	158	AspAsnAspIysValLeuIleGlnAspAsnPheSerThrGlyAspArgIysGlyAlaIleAsn	177
Db	430	AATTAATGAAAGTTCTCATTTCTATTAGTAATTTAGTCTCTGGAGATGGGGAGCTATAGAT	489
QY	178	CysAlaGlySerLeuIysIle-----	184
Db	490	---GCTTAAGCTTAAAGCTTCAAGAAATTAGCAAGCTTTGTGCTTCCAAAGAAATAACT	546
QY	185	-----AlaAsnAsn	187
Db	547	GCTCAAGCTGATGGGGAGCTTGCAATAGTCAACAGTTTCTGCTATGGCTTAACGAG	606
QY	188	LysSerLeuSerPheIleGlyAsnSerSerSerThrArgGlyAlaIleIleThr---	206
Db	607	GCTCTATTGCTTTGTATGCGAATGTTTCAGAGAGTAAAGGGGAGAGGATGTGCTGCTT	666
QY	206	-----	206
Db	667	CAGATGGGAGAGAGAGTGCATCATCTTCAACAGAAATCCAGTAGTAAGTTT	726
QY	206	-----	206
Db	727	TCCAGAAATACGCGGTAGATTGTGATGGAAAGTAGCCGAGTAGAGAGAGGATTTAC	786
QY	207	-----LysAsnLeuThrLeuSerSerGlyGlyIuThrLeuPheGlnGlyAsnThrAla	224
Db	787	TCTACGGGAGACGTTCTTCTCTGAATAATGAAAAACCTTGTTTCTCAACAATGTTGCT	846
QY	225	-----ProThr-----	226
Db	847	TCTCTGTTTACATTTGCTGCTAAGCAACAACAAGTAGAGCAGGCTTCAATACGATTAAT	906
QY	226	-----	226
Db	907	AATTACGGAGATGAGAGAGCTATCTTCTGTAAAGATGTGCGCAAGACAGATCCAAATAC	966
QY	227	-----AlaAla	228

Db 967 TCTGATCAGTTCTTGTATGAGAGGAGTAGTTTCTTATAGCAATGATGCT 1026
 QY 229 GYLYS----- 230
 Db 1027 GGGAAAGGGAGCTATTATGCAAAAGCTCTGGTTCATCTGGCCCTGACAA 1086
 QY 231 -----GlyGlyAlaIleAlaIleAspSerGlyThrLeu 242
 Db 1087 TTTTAAAGAAATATGCTAATATGATGAGAGATTTATTTAGAGAAATCTGGAGCTTC 1146
 QY 243 SerIleSerGlyAspSerGlyAspIleIlePheGly----- 255
 Db 1147 ACTTATCTGCTGATATGAGATATATTTCTGATGGAATCTTAAAGACAGCAAA 1206
 QY 256 ---AenThrIleGlyAlaThrGly---ThrValSerHisSerAlaIleAspLeuGlyThr 273
 Db 1207 GAGAAATGCTCCGATGTTAATGCGGTACCTGCTCTCAAGCCATTTTCATGAGGATG 1266
 QY 274 SerAlaIleIleThrAlaLeuArgAlaIleGlyIleIleThrIleGlyPheTyrosPro 293
 Db 1267 GGAGGAAATTAACACATTAAGAGCTTAAGACAGGACATCAATCTCTTAATGATCCC 1326
 QY 294 IleThrVal---ThrGlySerThrSerValAlaAspAla-----LeuAsnIleAsn 309
 Db 1327 ATCGAGATGCAAAAGCAATATACAGCAGCAGCAGCTTCCAAACTTCTTAAATTAAC 1386
 QY 310 SerProAspThrGlyAspAsnIleGlyIleThrGlyIleValPheSerGlyLeuIle 329
 Db 1387 -----GATGGTAAAGATACACAGGAGATATGTTTGTCT----- 1422
 QY 330 LeuThrGluAlaGluAlaIleAspGluIleAsnArgThrSerIleLeuLeuGlnAlaVal 349
 Db 1423 -----AATGAAAGCATCTTGTATCCAAATGTT 1452
 QY 350 AlaPheIleAsnGlyThrValIleLeuIleGlyAspValIleLeuSerAlaAsnGlyPhe 369
 Db 1453 ACGATATGCAAGCAAGGATGTTCTTCTGTAAGCAAAATTAATCACTGAAATCTCTA 1512
 QY 370 SerGlnAspAlaAsnSerIleLeuIleMetAspLeuGlyThrSerLeu----- 385
 Db 1513 AATCAGACAGTGGAGT---CTGTAATGCAAGCTGGAATACATTTGATTTGTAAT 1569
 QY 386 -----ValAlaAsnThrGluSerIleGluLeuThrAsnLeuGlu 398
 Db 1570 CCAACAACCAACAACAGCTCTGCTCCGCTAATCACTTAATCACTTCCAAATCTGAT 1629
 QY 399 IleAsnIleAspSerIleLeuArgAsnGlyIleValIle----- 410
 Db 1630 TTGTCTCTTCTTCTTGTAGCAACATGCAATGCAATGCAATCTCTCAATCTGCA 1689
 QY 411 -----LysLeuSerAlaAlaIleThrAlaGlnLysAspIleArgIleAsp 424
 Db 1690 GCGCAAGATTCTCATCTCGACATGATGTCAGCAACAATGCTGTTCTCTCAATTAAT 1749
 QY 425 ArgProValIleLeuAlaIleSerAlaAspSerArgSerIleAspAlaValIleSerPro 475
 Db 1750 GGGCCTATCTTTTTCAGATTTGATGATACAGCTTAATGAG----- 1794
 QY 445 AspHisSerTyrosPhe-----GlyIleLeuGlnLeuAspAla 456
 Db 1795 -----TATGATTTGGCTAGGATCTTAATCAAAATTAATGATGCTGTAATTAACGTTA 1845
 QY 457 GlyLysAspIleValIleSerAlaAspSerArgSerIleAspAlaValIleSerPro 475
 Db 1846 GGAGCTAAAGCCCGACCTAATGCCCATCATGATTTGACTCTAGGAAATGATGCTTAAG 1905
 QY 476 TyrGlyTyrGlnGlyIleThrIleAsnIlePheSerThrAspAspLys----- 491
 Db 1906 TATGCTATCAAGAGAGCTGGAAGCTTGGAGATCTTAATACAGCAAAATTAATGCTCT 1965
 QY 492 -----LysAlaThrValSerIlePheIleValGlnSerPheAsnProThrAlaGln 508
 Db 1966 TATACTCTGAAGCTACA-----TGAAGTAAATCGGGATATATCTCTGGGCTGAGCGA 2019

QY 509 GluAlaProLeuValProAsnLeuLeuThrGlySerPheIleAspValArgSerPheGln 528
 Db 2020 GTAGCTTCTTGTGGTCCAAATATGTTATGAGGATCCATTTTATATATACATCTCCGAT 2079
 QY 529 AsnPheIleGluLeuGlyThrGluGlyValaProTyrGlyIleValArgPheThrValaIleGly 548
 Db 2080 TCAGCAATTCAGCAAGATGATGAGGAGGCTTATGTCAGAGATTAATGAGGTTTCTGGA 2139
 QY 549 IleSerAsnValLeuHisArgSerGlyArgGluAsnGlnGlyPheArgHisValSer 568
 Db 2140 GTTTCGAATTTCTTCTATCATGACCGCATCTTATAGCTCAGGATATCGGATATATTAGT 2199
 QY 569 GlyGlyAlaValAlaGlyAlaSerThrArgMetProGlyGlyAspThrLeuSerLeuGly 588
 Db 2200 GGGGGTATTCCTTATGAGCAAACTCTTACTTT---GATCATCATGATGTTGGTCTACGA 2256
 QY 589 PheAlaGlnLeuPheAlaArgAspLysAspTyrPheMetAsnThrAsnPheAlaLysThr 608
 Db 2257 TTTACCGAAGATTTGATAGATCTTAAGATTAATGATGATGTCGTTCCAAATCATGATGCT 2316
 QY 609 TyrAlaGlySerLeuArgLeuGlnHisAspAlaSerLeuTyrSerValIleSerIleLeu 628
 Db 2317 TGCATAGGATCCGTTTATCTATCTAACCCACAGAGCTTATGAGA-----TCCATATTG 2370
 QY 629 LeuGlyGluGlyIleLeuArgGluIleLeuLeuProTyrValSerLysThrLeuProCys 648
 Db 2371 TTCGAGATGGCTTATTCGT----- 2391
 QY 649 SerPheTyrGlyGlnLeuSerTyrGlyHisThrAspHisArgMetLysThrGluSerLeu 668
 Db 2392 -----GCTAGCTAGCGGTTTGGAAATCAGCATATGAAACCTCATAT--- 2433
 QY 669 ProProProProThrThrLeuSerThrAsp---HisThrSerThrGlyGlyTyrValIle 687
 Db 2434 -----ACATTTGCAAGAGAGAGCGATGTTCTGAGTAATTAATCTGCTG 2478
 QY 688 AlaGlyGluLeuGlyIleThrArgValAlaIleGluAsnThrSerGlyArgGlyPhePheGln 707
 Db 2479 GCTGAGAGATTTGAGCGCGGATTAACCATGATGATTAATCTCAATCTTATTTGTAAT 2538
 QY 708 GluTyrThrProPheValIleValAlaGlnAlaValTyrAlaArgGlnAspSerPheValGlu 727
 Db 2539 GAGTTGCGCTCTTCTGTCGACAGCTGAGTTTCTTATGCGATCATGATCTTTTACAGAG 2598
 QY 728 LeuGlyAlaIleSerArgAspPheSerAspSerHisLeuTyrAsnLeuAlaIleProLeu 747
 Db 2599 GAAGCGATCAAGCTCGGGCATTCAGAGCGGACATCTCTTAATCTATCACTGCTCTGT 2658
 QY 748 GlyIleIleLeuGluIleValArgPheAla-----GluGlnTyrTyrHisValAlaIleMet 765
 Db 2659 GAGTGAAGATTGATGATGATGTTTATGATACATCTTAATTAATTAATGCTTTATGCGGCT 2718
 QY 766 TyrSerProAspValCysArgSerAsnProLysCysThrThrThrLeuLeuSerAsnGln 785
 Db 2719 TATATCTGATGCTTATCGACATCTCTGTCAGAGACAAACCTCTCTATCCATCA 2778
 QY 786 GlySerTyrPheThrLysGlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSer 805
 Db 2779 GAGCATGAGACAACAGATGCTCTTATTAACAGACATGAGTGTGTGATGAGAGACT 2838
 QY 806 GlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluIleThrArg 825
 Db 2839 ATGTATGCTTCTCTCAACAAGATTAATTAAGATTAATGCGCATGAGAAATATGATGATGA 2898
 QY 826 GlySerSerArgSerTyrAsnValaAspAlaGlySerLysIleLysPhe 841
 Db 2899 GATGCTTCTCAAGCTATGCTTATGATGTCAGAGATTAAGTCYGGTTC 2946

RESULT 9
 US-09-877-169
 ; Sequence 169, Application US/09556877
 ; Patent No. 6432916


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Db      1939 CACAGTTAGATGACCATCTTTCGCTGCGCAGAGCAATTAATCTCGGGAATCGTCC 1998
        598 AAPPYRPhemeAsnThrAsnPhenAlaIleValThrTyrAlaGlySerLeuArgLeuGlnHis 617
        1999 GATTCTTATTACTGCTACAGAAAGACCTCTTATATAGCTACTGCTACAGCGAATC 2058
        618 AepAlaSerLeuTyrSerValValSerIleLeuLeuGlyGlyLeuArgGluIle 637
        2059 GCTACCTCTCTAATGAAATCTGTGCA----- 2085
        638 LeuLeuProTyrValSerIleThrLeuProCysSerPheTyrGlyGlyLeuSerTyrGly 657
        2086 -----CAGCGATGCTACAT 2100
        658 HistHrAspHisArgMetLeuThrGlySerLeuProProProProThrLeuSerThr 677
        2101 GAAAGATCCAGATGAGCTAAACAAATAT-----CGCTCTTCTTAA 2145
        678 Asp---HisThrSerTyrGlyTyrValTyrAlaGlyGlyLeuGlyThrArgValAla 696
        2146 GAAAGATTCGATCCGATGCGATGCGTGAAGATCCGGAAGATGCGCATCGATCTCT 2205
        697 ValGluAsnThrSerGlyArgGlyPhePheGlnGlyTyrThrProPheValIleValGln 716
        2206 ATGTGA---TCCAAATGATCCGAGCTGTTCACTCTCTATTTCTCTAAACGCA 2262
        717 AlaValTyrAlaIleGlyAsnSerPheValGlyLeuGlyAlaIleSerArgAspPheSer 736
        2263 GAATTTTCAGAAACAGAGCGGTTTGAAGAGATTCGAGAGATTCGGTCCCTTTCT 2322
        737 AspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLysLeuGlyIleValArgPhe--- 755
        2323 GCGAGCTCTTCAAGAAATTTCACTCTCTATAGAAATACATTGAAAAAATCCCA 2382
        756 ---AlaGluGlnTyrTyrHisValValAlaMetTyrSerProAspValCysArgSerAsn 774
        2383 AAACAGCAACCTACTATTAATCTTCTAGAGAGCTTACCAAGCAACCTGAATGTG 2442
        775 ProLysCysThrThrThrLeuLeuSerAsnGlnGlySerTyrIleThrIleValSerAsn 794
        2443 GAATCGGAGCTGATGCTTACTCAAAATGCCGTTCTCGGAGTCTCTTAAGCGAAC 2502
        795 LeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAla 814
        2503 TTGGATTCAGAGCCACATGTTCCGCTTACGAATCAAGAGCTTACAGACTTCAG 2562
        815 GluLeuPheGlyAsnPheGlyPheGluTyrPargGlySerSerArgSerTyrAsnValAsp 834
        2563 ACCGTGTTA---AATGTGCTTGTGTGCTGCGCGGCAAGCATGTTACTCCCTGAT 2619
        835 AlaGlySerIleValSerPhe 841
        2620 CTGGGAGCACTTACAGGTTCT 2640

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RESULT 10
US-09-620-412C-169
; Sequence 169, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; LENGTH: 2643
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-169

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Alignment Scores:
Pred. No.: 1,766-66 Length: 2643
Score: 711.50 Matches: 241
Percent Similarity: 44.75% Conservative: 138
Best Local Similarity: 28.45% Mismatches: 347
Query Match: 16.57% Indels: 121
DB: 4 Gaps: 31
US-09-830-446-27 (1-841) x US-09-620-412C-169 (1-2643)

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QY	41	SerThrThrSerPheSerSerIleThrSerAlaThrAspGlyThrAsnTyrValPhe	60
DB	325	TCCTTCACAGATGTCCTTCCAGAGAACTCT	357
QY	61	LysAspSerValValIleGluAsnValProLysThrGlyIleThrGln	76
DB	358	---CCTTATTATTCATCA-----AAGATGGTCACTTCTCGCGCAATAT	405
QY	77	---SerThrSerCysPheLysAsn-----AspAlaAlaIleGlyAsp	89
DB	406	GGTACGATGATTTCTGTGCAATCATGCTGAGGCTGAGAGCATCTCGCGAT	465
QY	90	LeuAsnPheLeuGlyGlyGlyPheSerPheThrPheSerAsnIleAspAlaThrAla	109
DB	466	GCTTTTCTTACAGACACACTATCTTTCAAGCTTTGAAGAAATCTTCTTAAAGA	525
QY	110	SerGlyAlaAlaIleGlySerGlyAlaAlaAsnLysThrValThrLeuSer---GlyPhe	128
DB	526	AATGGCGAGCCATTCAGGCTCA-----ACCTTCTTTTATTAAGAAATGTG	573
QY	129	SerAlaLeuSerPheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIle	148
DB	574	TGCGCTATTCTTCTGCGCGTAAATGTCGGAT-----TTAAATGGC---GGCGTATT	624
QY	149	AsnValLysGlyAsnLeuSerLeuLysAsnAspLysValLeuIleGlnAspAsnPhe	168
DB	625	---TCGCTAGTAATCTTATTGTTCAAGGAATGAAACCTCTCTTTTCACTGAAAC	681
QY	169	SerThrGlyAspGlyGlyAlaIleAsnCys-----AlaGly	180
DB	682	TCGCGCAGAAAGGAGGCTATTTGTTGATACCGATCTTAAACACTCAGAAAAAGCG	741
QY	181	SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerThrArg	200
DB	742	TCTCTCTCTCTGCTTGAACCAAGAACGATTTGCAAGAAATCTGCTAAAGAAAA	801
QY	201	GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln	220
DB	802	GCGGGGCTATTATGCAAGCAATGATGATGCTTAAACGGTCTGTTCTTCAAT	861
QY	221	GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAspSerGly	240
DB	862	AACACACGCGCTAAATA-----GGTGAAGCTATGCGCATCCAGTCCGAGAGG	909
QY	241	ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThr-----Ile	258
DB	910	ACTCTCTATCTTCCAGCTGATGATGCTTCTTCCAGAAATACCTCCAGAGCACC	969
QY	259	GlyAlaThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThr	278
DB	970	TCGACCAAGGCTAGTA---AGAAACCCATCTCTTAAAGAAAGATCGGATTTCT	1026
QY	279	AlaLeuAspAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrGly	298
DB	1027	TCCTTAAGAGCTCGCAACGGA---GATATCTTCTTGTGATCTTAAT---GTACAGAA	1080
QY	299	SerThrSerValAlaAspAlaLeu-----AsnIleAsnSerPro--- 311	
DB	1081	AGTACAGCAAGAAATGCGCTTCTCCCTCTTGAAGCAGGATGCTCTCCACC	1140
QY	312	-----AspThrGlyAspAsnLysGlyIleThrGlyThr 322	

OY	403	SeTLeuAArgenGlyLyLeuVAlleuSerLeuSerLalathRlaaGlnLyAspIleArg	422
Db	1423	TcCTTAATACtGTAAGAAAGGGTAACTACTACAGCC-----CCTAACTTCT	1470
OY	423	IlleAspArgProValleuAlaIleSerAspGluSerPheTyrglnAsn--GlyPhe	441
Db	1471	ATCCAAAGATCTTCCTCCTCAACTCGAGATGAGAAATTATGAAATATGTAGACTT	1530
OY	442	LeuAnGluAepHisSerTyraSpGlyIleLeuGlnLeuAaplaGlyLyAspIleVal	461
Db	1531	CTCAGTAAAGCAGAAACAATATTCCTCCTCACTCCTCCTTAAGAGCAATCCATTTA	1590
OY	462	IlleSerIlaAspSerArgSerIleAspAlaValGlnSerProTyrglyTyrglnGlyLy	481
Db	1591	CATCTCTCTGATGGGAAC-----CTCTCTTCTCACTTGATGATCAAGAGAT	1638
OY	482	TrpThrIleAsnTrpSerThrAspAspLys-----LysAlaThrValSerTrpAlaLys	499
Db	1639	TGGACTTTCTTGGAAGATTCGTATGAGAGGCATCTCGATTGCTAATGTGACGCT	1698
OY	500	GlnSerPheAsnProThrIlaGlnGlnLualaProLeuValProAnLeuLeuTrpGly	519
Db	1699	AAAAACAATGCTCCTCATCCAGAACGCAATCACTCACTCGTGGAAACACTTTTGAAC	1758
OY	520	SerPheIleAspValaArgSerPheGlnAsnPheIleGluLeuGlyThrGlnGlyAlaPro	539
Db	1759	ACCATTCCTCGATATGCAAGCTGTGCATGATCAATTAACAAGAGCGACGGAGAGCC	1818
OY	540	TyrGlnLysArgPheTrpValaIleGlyIleSerAnVal-----LeuHisArgSerGly	557
Db	1819	TATCATTTTGGAGAGTGGGGAGTGTGCTTTCTAATTTATTTCAATGTATCAAGAGCTCT	1878
OY	558	ArgGlnAnGlnaArgLysPheArgHisValSerGlyGlyAlaValaIleGlyAlaSerThr	577
Db	1879	GGGAAACCTATGCATTAATGGCATCATAGAGCCTTGGCTACCTATTCCGATACAGTACT	1938
OY	578	ArgMetProGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLys	597
Db	1939	CACAGTTTAGATGACCAATCTTCTGTGCTGGCTCAGAGACAATTAATCCGGAAATCTGC	1998
OY	598	AspTyraPheMetAnThrAnAsnPheAlaLysThrTyraIleGlySerLeuArgLeuGlnHis	617
Db	1999	GATTCCTTATTAAGCTGCACAGAAACGACCTCTCATTAAGCTACTGTACAAAGCGCACTC	2058
OY	618	AspAlaSerLeuTyraSerValaSerIleLeuLeuGlyGlnGlyGlyLeuArgGlnIle	637
Db	2059	GCTACCTCTCAAGAAATACTCGCA-----	2085
OY	638	LeuLeuProTyraLysLysThrLeuProCysSerPheTyrglyGlnLeuSerTyrgly	657
Db	2086	-----CAGGACGTCTACAT	2100
OY	658	HisThrAspHisArgMetLysThrGlnSerLeuProProProThrLeuSerThr	677
Db	2101	GAAAGTATCCATGAGCTAAACAAATAAT-----CGTCTCTCTCAAA	2145
OY	678	Asp--HisThrSerTrpGlyGlyTyraValTrpAlaGlyGlnLeuGlyThrArgValaIa	696
Db	2146	GAGAGATTCGAGTCTGGCATAGCGTTTCAGATACCGGAGAAAGTGGCGCATCAATTCCT	2205
OY	697	ValaGlnAnThrSerGlyArgGlyPhePheGlnLeuTyraThrProPheValLyValGln	716
Db	2206	ATTGTA--TCCAAATGTTCCGAGCTGTACGCTCTCTCAATTTCTCAAACTGCA	2262
OY	717	AlaValTyraLysArgGlnAspSerPheValGlnLeuGlyAlaIleSerArgAspPheSer	736
Db	2263	GGATTTCAGAAACACAGACGATTTTGAGAGAGTTCGGAGAGATTCGATCTCTTCT	2322
OY	737	AspSerHisLeuTyraLeuLeuAlaIleProLeuGlyIleLysLeuGlnLysArgPhe---	755
Db	2323	GCCAGCTCTTTCAGAAATATTTCACTCTCTTAATGAGAAATTAATTTGAAAAAAATCCCA	2382

QY 756 ---AlGIuGIuInTyThrYHseValAlaMeTySerProApValCybatgSerAan 774
 Db 2383 AAAACGACGAACCTACTATTAATCTTACGAGCCTTACATCCAAAGCTGAATGTG 2442
 QY 775 ProLySeThrThrThreuleuSerAanGInGlySerThyThrYHseVal 794
 Db 2443 GAATGGGAGCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2502
 QY 795 LeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAla 814
 Db 2503 TTGGATTACGAGCCTTACATGTTCCGGCTTACAAATCAAAGACTTACAGACATTCAG 2562
 QY 815 GluLeuPheGlyAanPheGlyPheGluThrPargGlySerSerArgSerThyAanVala 834
 Db 2563 ACCGCTGTA---AATGTGCTTGTGTGCTGCGGCAAGCATGATGATGATGATGAT 2619
 QY 835 AlaGlySerIleValIleValPhe 841
 Db 2620 CTGGGAGCACTTACAGGTTG 2640
 RESULT 12
 US-09-556-877-181
 ; Sequence 181, Application US/09556877
 ; Patent No. 6432916
 ; GENERAL INFORMATION:
 ; APPLICANT: Probet, Peter
 ; APPLICANT: Bhatia, Ajay
 ; APPLICANT: Skeiky, Yashir
 ; APPLICANT: Piling, Steve
 ; APPLICANT: Malsomene, Jeff
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
 ; FILE REFERENCE: 210121.469C5
 ; CURRENT APPLICATION NUMBER: US/09/556,877
 ; CURRENT FILING DATE: 2000-04-19
 ; NUMBER OF SEQ ID NOS: 305
 ; SOFTWARE: FastSeq for Windows Version 3.0/4.0
 ; SEQ ID NO 181
 ; LENGTH: 2601
 ; TYPE: DNA
 ; ORGANISM: Chlamydia
 US-09-556-877-181
 Alignment Scores:
 Pred. No.: 7,19e-65 Length: 2601
 Score: 696.50 Matches: 238
 Percent Similarity: 44.27% Conservative: 137
 Best Local Similarity: 28.10% Mismatches: 351
 Query Match: 16.22% Indels: 121
 Gaps: 31

QY 129 SerAlaLeuSerPheLeuLysSerProAlaSerThrValThraSerGlyLeuGlyAlaIle 148
 Db 532 TCGCCATTTCTTTTCCGCCATATCGCCGAT-----TTAAATGGC---GGCCGTATT 582
 QY 149 AanValIleGlyAanLeuSerLeuLeuAanAanValIleGlnAanPhe 168
 Db 583 ---TGGTGTAGTAATCTTATTGTTTTCAGGAATGTAAACCTCTCTTTTCACTGGAAC 639
 QY 169 SerThrGlyAanPheGlyValAlaIleAanCys-----AlaGly 180
 Db 640 TCCGCCACAAATGAGAGCGCTATTGTTGATCAGCATCTAAACCTCAGAAAAAGCG 699
 QY 181 SerLeuLysIleAlaAanAanLysSerLeuSerPheIleGlyAanSerSerThra 200
 Db 700 TCTCTCTCTCTGCTTGTATCAABAACGATATTGCAAGAAATCTCTAAAGAAAA 759
 QY 201 GlyValAlaIleHisThrYHseLeuThrLeuSerSerGlyGluThrLeuPheGln 220
 Db 760 GGCGGGGCTATTATGCAAGACATGATGCGTTATTAACGCTCGTTCTTCATT 819
 QY 221 GlyAanThraIleProThraIleAlaGlyIleValAlaIleAlaAanSerGly 240
 Db 820 AACAAACAGCGTAAATA-----GGTGAAGCATATGCCATCCAGTCGGAGCG 867
 QY 241 ThrLeuSerIleSerGlyAanPheGlyAanIleIlePheGlyAanThr-----Ile 258
 Db 868 AGCTCTCTATCTTGTGAGTGAAGATCTGTTGTTCCAAATTAATCCCAAGCAGCACC 927
 QY 259 GlyAlaThrGlyThraValSerIleAlaAanPheGlyThraSerAlaLysIleThr 278
 Db 928 TCCGACCAAGGCTTAGTA---AGAAACGCATCTACTTAGAAGAAAGTCGATCTTCT 984
 QY 279 AlaLeuArgAlaAlaGlnGlyHisThrThyIlePheYHseProIleThraValThrGly 298
 Db 985 TCTTGAAGCTCGCAACGA---GATATCTTCTTGTGATCTTAT---GTACAGAA 1038
 QY 299 SerThraSerValAlaAanPheLeu-----AanIleAanSerPro--- 311
 Db 1039 AGTAGAGCAAGAAATCGGCTTCTCCCTCTTTCGACCAAGCGTACTTCCACACC 1098
 QY 312 -----AanThrGlyAanPheLysGluThrGlyThr 322
 Db 1099 CCAGCCACCGCATCTCTTATGTTATTCAGACAAATGCAAAACCGT-----TCA 1146
 QY 323 IleValPheSerGlyGluLysLeuThrGlnAlaGlnAlaAanPheLysAanArgThr 342
 Db 1147 GTGATTTCTCGAGGAACGCTTCTGA---GAAGAAAAAACTCTGATTAACCTCAGCT 1203
 QY 343 SerLysLeuLeuGlnAanValAlaPheLysAanGlyThraValIleLysGlyAanVal 362
 Db 1204 TCCCAACTAGACAGCCTATTCGAATCGAAATCCGACGCTTATTAAAGATCGCGCT 1263
 QY 363 ValLeuSerAlaAanGlyPheSerGlnAanPheAanSerLysLeuIleMetAanPheGly 382
 Db 1264 GTCCTTCCGSCCTTCTCTCTCAGATCTCAAGCTCTCTCATATGGAAGCGGGA 1323
 QY 383 ThrSerLeuValAlaAanThrGlnSerIleGluLeuThraAanLeuGlnIleAanIleAan 402
 Db 1324 ACTTCTTTAAAACTTCTCTTAT---TTGAAGTAGTAGCTAGTATTCCTCTCAT 1380
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 Db 1381 TCTTATGATCTGAAGAAAGCTAATCTACAGCC-----CTTATCTTCT 1428
 QY 423 IleAanArgProValValLeuAlaIleSerAanPheLysPheThraAan---GlyPhe 441
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 QY 442 LeuAanGluAanPheIleSerThraPheGlyIleLeuGluLeuAanPheAlaGlyAanIleVal 461
 Db 1489 CTCAGTAAAGCAAAACAAATATTCCTCTTACTCTCCCTAAAGCAATCTCATTTA 1548
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Db      1549 CATCTCCGATGGGAC-----CTCTCTCTCACTTGGATATCAAGAGAT 1596
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Db      1597 TGGACTTTTCTTGAAGATTCTATGTAAGGCAATCTCTGATGTTGTAAGCGCT 1656
Qy      500 GlnserPheasnProThralaglIngluaIaProleuValProAsnleuThrpoly 519
Db      1657 AAAAATACTATGCTCATCCAGACAGCTCATCTACCTCTTGGCAACCTTTGGAAC 1716
Qy      520 SerPheileaspValaArserPheglInasnPheilegluLeuglyThrcIuIyalaPro 539
Db      1717 ACCTATTCGATATCAAGCTGAGCTGATGATTAATACAAAGCGAGAGAGAGCC 1776
Qy      540 TTTGluIyAaPhetTPValaIaIyIleSerAenVal-----leuHleArsergly 557
Db      1777 TATCTATTGGAACCGGAGACTCTCTGTTCTTAATTATCTATGTTTCAACAGAGCTCT 1836
Qy      558 ArggluaInglInArglyPheArghIseValserglyIyalaIvalaIyalaIserThr 577
Db      1837 GGGAAACCTATCGATATATGGATCGATAGAACCTTGGCTACTTATCGATATCACTACT 1896
Qy      578 ArgMetProglyIyAspThrleuSerleuglyPheAlaglInleuPheAlaArghApy 597
Db      1897 CACAGTTAGATGACCATCTTCTGCTGCTGAGAGCAATTACTGGGAATCGTCC 1956
Qy      598 AApTYrPheMetAsnThrasPheAlaIyThrTYrAlaIySerleuArghleuInHis 617
Db      1957 GATTCTTATTAACCTCTACAGAAAGCAACCTCTTATATGACTACTGACAGCGAGACTC 2016
Qy      618 AepAlaSerleuTYrSerValaIserIleleuLeuIygluIygluLeuArghIurle 637
Db      2017 GCTACTCTCTATATGAATAATCTCTGA----- 2043
Qy      638 leuLeuProTYrValserIyThrleuProCYserPheTYrGlyInleuSerTYrly 657
Db      2044 -----CAGCAGATCGTACAT 2058
Qy      658 HleThrasPheHleArghMetIyThrcIuSerleuProProProProThrleuSerThr 677
Db      2059 GAAATATCCATGACGCTAAACAAATAT-----CGCTCTCTCTTAA 2103
Qy      678 Aep---HleThSerTrpolyIyTYrValTYrAlaIygluLeuIyThraArghVala 696
Db      2104 GAAAGATTCGATCTCGGATAGCGCTGCAAGATCCGAGAAAGTGGCCATCATCTCT 2163
Qy      697 ValgluaInThrSerIyArghIyPhePheglInIyTYrThProPheValIyValaIy 716
Db      2164 ATTTGA---TCAATGATTCGAGATGTTCACTCTCTATTTCTCTAAATCGCA 2220
Qy      717 AlaValTYrAlaArghInaPserPheValgluLeuIyAlaIleSerArghApySer 736
Db      2221 GAATTTTCAGAAACAGAGCGATTTTGAAGAGATTCGAGAGATTCGATCTCTTCT 2280
Qy      737 AepSerHleuTYrAsnleuAlaIleProleuIyIleIyLeuIygluIyArghPhe--- 755
Db      2281 GCGAGCTTTCAAAATATTTCACTCTCTATAGAAATACATTTGAATAAAATCCCA 2340
Qy      756 ---AlaIygluIyTYrHleValaIaIeTYrSerProApyValCYarSerAen 774
Db      2341 AAAACAGAACTCATATTACTTTAGAGAGCTACATCAAGAGCTGAAGAGTATG 2400
Qy      775 ProIyScyThrThrleuIeuserAngInIySerTPlyThrIySerIySerAen 794
Db      2401 GAATCGGAGCTGTAGTGTACTCAAAATGCGCTCTCTGAGATGCTCTATGCGAAC 2460
Qy      795 leuAlaArghInaIaIyIleValaIaIeSerIyPheArghSerleuIyAlaIaIa 814
Db      2461 TTGATTCAGAGCTCAATGTTCCGCTTACGAATCAAGAGCTTACAGAGACTTCA 2520
Qy      815 GluIeupheglIyAsnPhetIyPhegluIyPargIySerSerArghSerTYrAenValAep 834

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Db      2521 ACCTGTTA---AATGTCCTTGTCGTGCGTGGGAAACCATATGTACTCCCTGAT 2577
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Db      2578 CTGGGAGCACTTACAGGTTC 2598

RESULT 13
US-09-620-412C-181
; Sequence 181, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 181
; LENGTH: 2601
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-181

Alignment Scores:
Pred. No.: 7,19e-65 Length: 2601
Score: 696.50 Matches: 238
Percent Similarity: 44.27% Conservative: 137
Best Local Similarity: 28.10% Mismatches: 351
Query Match: 16.22% Indels: 121
DB: 4 Gaps: 31

US-09-830-446-27 (1-841) x US-09-620-412C-181 (1-2601)
Qy      41 SerThrThrSerPheSerSerIyThrSerSerAlaThraApyIyThraAntyValPhe 60
Db      283 TCCCTTACAGATGCTGCTTCCAGAAAGCTCT----- 315
Qy      61 LyAaPserValaIleIygluAenValProIySerThrcIuIyThrcIn----- 76
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Qy      77 ---SerThrSerCyPheIyAasn-----AepAlaIaIaIyAsp 89
Db      364 GGTACATGATGTTCTGCAAAATCATCTGAAGCTTGAGAGAGCATCTCGGAT 423
Qy      90 leuAsnPhleuIyglIyglIyPheSerPheThrPheSerAenIleApyAlaThrAla 109
Db      424 GCTTTTCTTACAGACAACTATCTTTCAAGCTTTGAAGAAATTTCTTAAGGA 483
Qy      110 SerIyAlaIaIaIeIySerIyAlaIaIaIyThrValIyThrleuSer---GlyPhe 128
Db      484 AATGCGGAGCATTCAGCTCA-----ACCTTCTTTATCTAAGAAATG 531
Qy      129 SerAlaIeuserPheleuIySerProIaSerThrValThraAngIyLeuIyAlaIle 148
Db      532 TCGCTATTCTTTGCGCCGTAATCGTCGAT-----TTAAATGCG---GGCGTATT 582
Qy      149 AasnValIyglIyAasnleuSerleuIyAasnApyValleuIleIyIaAsnApy 168
Db      583 ---TGTCTAGTAATCTATTATTGTCAGAGAAATGAACCTCTCTTTTTCAGTGAAC 639
Qy      169 SerThrcIyAaPglIyAlaIleAenCYs-----AlaIy 180
Db      640 TCCGCGCAATGAGAGGCTATTGTTGATCAAGCATTAACACCTCAGAAAAAGGC 699
Qy      181 SerleuIyIleAlaAsnIySerleuSerPheIleIyAasnSerSerThraArg 200
Db      700 TCTCTCTCTCTGTTGACCAAAACGCTATTGACCAATTTCTGCTAAAGAAAA 759
Qy      201 GlIyAlaIaIeIyThrIyAasnleuThrleuSerSerIyglIygluIyThrcPheglIn 220

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Db 760 GCGGGGCTATTATGCGAAGCAGTGTATGCGTTATACGGCTCTGTTCTTCAT 819
 Qy 221 G1yAsnThrAlaProThrAlaAlaGlyGlyValAlaIleAlaIleAspSerGly 240
 Db 820 AACAGACGCCCTAAATAT-----GATGACCTATTCGCAATCCAGTCGAGG 867
 Qy 241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThr-----Ile 258
 Db 868 AGTCTCTATCTCTGCGAGGTGAAGATCTGTTCTGTTCCAGAAATATCCCAACGAC 927
 Qy 259 G1yAlaThrGlyThrValIleSerIleSerAlaIleAspLeuGlyThrSerAlaGlyIleThr 278
 Db 928 TCCGACCAAGGTCTAGTA---AGAAAGCCATCTACTATGAGAAAGATGCAATCTTCT 984
 Qy 279 AlaLeuThrGlyAlaAlaGlnGlyIleThrIleThrPheThrAspProIleThrValIleThrGly 298
 Db 985 TCTTATAGAGCTGCAACGGA---GATATCTTCTTATGATCTAT---GATCAAGAA 1038
 Qy 299 SerThrSerValAlaAspAlaLeu-----AsnIleAsnSerPro--- 311
 Db 1039 AGTAGAGCAAGAAAGATGCGCTTCTCCTCTTTCGACAGCAGCGTCTTCCAC 1098
 Qy 312 -----AspThrGlyAspAsnGlyGlyThrGlyThr 322
 Db 1099 CCAAGCCACCGATCTCCTTATGATATGACAGAAAGTCAAAACGT-----TCA 1146
 Qy 323 IleValPheSerGlyGlyIleuThrGluAlaGlyAlaIleAspGlyIleAspAsnThr 342
 Db 1147 GTGATTTCTGAGCGAAGCGTCTTCTGAA---GAAAGAAAGCTCTGATTAACCTCACT 1203
 Qy 343 SerIleuLeuGlnIleAsnValAlaPheIleAsnGlyThrValIleuLeuGlyAspVal 362
 Db 1204 TCCCAACTACAGAGCTATGCAAGTGAATCCGAGCGCTTATGTTAAAGATCCGCT 1263
 Qy 363 ValLeuSerAlaAsnGlyPheSerGlyAspAlaAsnSerIleuIleMetAspLeuGly 382
 Db 1264 GTCTTTCGCGCTCTCTCTCTCAGAGATCTCAAGCTCTCAATTAAGAAAGCGGA 1323
 Qy 383 ThrSerIleuValAlaAsnThrIleuSerIleGluIleuThrAsnLeuGluIleAsnIleAsp 402
 Db 1324 ACTTCTTAAAGATCTCTTGTAT---TTGAGTTAGTACGATTAATATTCCTTCAT 1380
 Qy 403 SerIleuThrAsnGlyIleuIleuSerIleuIleuSerAlaIleThrAlaGlnIleAspIleArg 422
 Db 1381 TCTTATGATCTGAAAGACGTATCACTACAGCC-----CCTAATCTTCT 1428
 Qy 423 IleAspArgProValAlaIleuAlaIleSerAspGlySerPheThrGlnAsn---GlyPhe 441
 Db 1429 ATCCAAAGATCTTCTCTCTAATCTGAGATGAGATTTTATGAAATATGAGACTT 1488
 Qy 442 LeuAsnGluAspIleSerIleuAspGlyIleuGluIleuAspAlaGlyIleAspIleVal 461
 Db 1489 CTGAGTAAAGCAAAACATATATCTCTCTAATCTCTCTAAGCAATCTCAATTA 1548
 Qy 462 IleSerAlaAspSerIleAspAlaIleGlnSerProGlyThrGlnIleGly 481
 Db 1549 CATCTTCTGATGGAAC-----CTCTCTCTCACTTGTGATATCAAGGAGAT 1596
 Qy 482 TrpThrIleAsnTrpSerThrAspAspIle-----LysAlaThrValSerTrpAlaIle 499
 Db 1597 TGGACTTTTCTTGAAAGATCTGATGAGGCAATCTCTGATGCTAATGAGAGCCT 1656
 Qy 500 GlnSerPheAsnProThrAlaGlnGlnIleuAlaProLeuValIleProAsnLeuLeuTrpGly 519
 Db 1657 AAAAAGATATGCTCTATCCAGAACGTCATCACTCTCTGCAACCTCTTGGAC 1716
 Qy 520 SerPheIleAspValIleAspPheGlnAsnPheIleGluLeuGlyThrGlnIleAlaPro 539
 Db 1717 ACTATTCGATATGCAAGCTGTCAGCTCATATTAATCAACAGCGCAGAGAGACC 1776
 Qy 540 TyrGluIleAspThrTrpValAlaGlyIleSerAsnVal-----LeuIleAspSerGly 557
 Db 1777 TATCTATTGAAAGTGGGATCTGCTTCTAATTAATTAATTAATGTTCAAGACGCT 1836

Qy 558 ArgGluAsnGlnIleArgIlePheArgIleValIleSerGlyValAlaValAlaSerThr 577
 Db 1837 GGGAAACCTATCATTAATGCAATCATAGAGCTTGGCTACTTATCCGTATCAAGTACT 1896
 Qy 578 ArgMetProGlyGlyAspThrIleuSerIleuGlyPheAlaGlnIleuPheAlaArgAspIle 597
 Db 1897 CACAGTTATGATGACCATCTTCTGCTTGTGAGAGCAATTAATCTCGGAAATCGTCC 1956
 Qy 598 AspThrPheMetAsnThrAsnPheAlaIleThrIleAlaGlySerIleuArgLeuGlnIle 617
 Db 1957 GATTCCTTATTAATGCTATCAGAAAGCACTCTATATAGCTATGATACAGGCAATC 2016
 Qy 618 AspAlaSerIleuThrValIleSerIleuLeuGlyGluGlyIleuArgGluIle 637
 Db 2017 GCTACTCTCTAATGAAATCTCTGCA----- 2043
 Qy 638 LeuLeuProThrValIleSerIleuProCysSerPheThrGlyGlnIleuSerThrGly 657
 Db 2044 -----CAGGCACTCAAT 2058
 Qy 658 HisThrAspHisArgMetIleThrGluSerLeuProProProThrIleuSerThr 677
 Db 2059 GAAAGTATCCATGACGTAAACAAATAT-----CGCTCTCTCTA 2103
 Qy 678 Asp---HisThrSerThrGlyIleThrValIleThrAlaGlyIleuGlyThrArgValAla 696
 Db 2104 GAAAGATTCGAGATCTGCGATGACCTTGCAGTATCCGAGAGATGCGCATGATCTCT 2163
 Qy 697 ValGluAsnThrSerGlyIleArgIlePhePheGlnGlyThrIleProPheValIleGln 716
 Db 2164 ATGTA---TCAATGATTCGAGCTGTTAGCTCTCTCTATTTCTCTAATCGCA 2220
 Qy 717 AlaValThrAlaArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSer 736
 Db 2221 GATTTTCAGAAACAGACGCTTTTGAAGAGTTCGAGAGATTCGCTCTTCT 2280
 Qy 737 AspSerHisLeuThrAsnIleAlaIleProGlyIleIleuGlyIleuAspPhe--- 755
 Db 2281 GCCAGCTCTTCAAGAAATATTCATCTCTATGAGAAATCAATTAAGAAATATCCAA 2340
 Qy 756 ---AlaGluGlnIleThrIleValAlaIleMetIleSerProAspValCysArgSerAsn 774
 Db 2341 AAAACAGAACCTACATTAATCTTACAGAGCTTACATCAAGCTGAAGCTGATG 2400
 Qy 775 ProIleCysThrThrIleuLeuSerAsnGlnIleSerThrIleThrIleGlySerAsn 794
 Db 2401 GAATCGGACCTGATGTTACTCAAAATATGCGCTCTCGGATGCTCTATGCGGAAC 2460
 Qy 795 LeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerIleuGlyAlaAla 814
 Db 2461 TTGATTCAGAGCTGATGTTCCGCTTACCAATCAAGAGCTTACACAGACTTCAG 2520
 Qy 815 GluLeuPheGlyAsnPheGlyPheGluThrArgGlySerSerArgSerThrAsnValAsp 834
 Db 2521 AGCTGTTA---AATGCTCTGTGCTGCTGCTGCGCAAGCATATGTTATCCCTGAT 2577
 Qy 835 AlaGlySerIleuLysPhe 841
 Db 2578 CTGGGAGCACCTTACAGTTT 2598

RESULT 14
 US-09-598-419-181
 ; Sequence 181, Application US/09598419
 ; Patent No. 6565856
 ; GENERAL INFORMATION:
 ; APPLICANT: Skelley, Yasir A.W.
 ; APPLICANT: Scholler, John
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
 ; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
 ; FILE REFERENCE: 210121.46906
 ; CURRENT APPLICATION NUMBER: US/09/598,419
 ; CURRENT FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 357
 SOFTWARE: FASTSEQ for Windows Version 3.0/4.0
 SEQ ID NO: 181
 LENGTH: 2601
 TYPE: DNA
 ORGANISM: Chlamydia
 US-09-598-419-181

Alignment Scores:

Pred. No.:	7,196-65	Length:	2601
Score:	696.50	Matches:	238
Percent Similarity:	44.27%	Conservative:	137
Best Local Similarity:	28.10%	Mismatches:	351
Query Match:	16.22%	Indels:	121
DB:	4	Gaps:	31

US-09-830-446-27 (1-841) x US-09-598-419-181 (1-2601)

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DB 283 TCCTTCACAGATGCTCTTCCAGAGAAAGCTCT----- 315
QY 61 LysAspSerValValIleGluAsnValProlySerGlyGluThrGln----- 76
DB 316 ---CCCTTATATTCATCA-----AAGATGTCAGTTATCCTTGCGCAATAT 363
QY 77 ---SerThrSerCysPheLysAsn-----AspAlaAlaIleGlyAsp 89
DB 364 GGTACACAGATGTTCTGCGAATATCATGCTGAAGCTCTGAGAGAGCCATCTCGGAT 423
QY 90 LeuAsnPheLeuGlyGlyIlePheSerPheThrPheSerAsnIleAspAlaThrAla 109
DB 424 GCCTTTCCTACAGACACATATCTTTTACAGCTTTGAGAGATCTCTTAAGCA 483
QY 110 SerGlyAlaAlaIleGlySerGluAlaAlaAsnLysThrValThrLeuSer--GlyPhe 128
DB 484 AATGCGAGGACCATTCAGGCTCA-----ACCTTCTTATCTGAATATG 531
QY 129 SerAlaLeuSerPheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIle 148
DB 532 TCGCTATTTCTTGCCCGTAAATCGTCGGAT-----TTAAATGCG--GCGCTAT 582
QY 149 AsnValLysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsn 168
DB 583 ---TGCTGAGATATCTTATTTGTCAGGGAATGAACCTCTCTTTTACCTGGAAC 639
QY 169 SerThrGlyAspGlyGlyAlaIleAsnGlyS-----AlaGly 180
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QY 181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerThrArg 200
DB 700 TCTCTCTCTGCTGTTGAACCAAAACGTAATTTGACAGCAATTCCTTAAGAAAA 759
QY 201 GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyIleThrLeuPheGln 220
DB 766 GCGGGGCGCTATTATGCCACAGCATGATTCGCTTAACGGTCCTTTCTTCATT 819
QY 221 GlyAsnThrAlaProThrAlaAlaGlyGlyGlyAlaIleAlaIleAspSerGly 240
DB 820 AACCAACAGCGCTAAATA-----GGTGAAGCTATCGCCATCCAGTCGGAGGG 867
QY 241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThr-----Ile 258
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DB 928 TCCGACCAAGGCTGATAT---AGAAAGCGCATCTACTTAGAGAAATGCAATCTTCT 984
QY 279 AlaLeuArgAlaAlaGlnGlyHisThrIleTyPheTyAspProIleThrValThrGly 298
DB 985 TCTTAGAAGCTCGCAACGGA---GATATCTTTCTTGATCTTAT---GTACAAAGA 1038
  
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QY 299 SerThrSerValAlaAspAlaLeu-----AsnIleAsnSerPro--- 311
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QY 312 -----AspThrGlyAspAsnLysGluTyThrGlyThr 322
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DB 1147 GTGATTTCTGAGCGAAGCGTCTTCTGAA---GAAGAAAAAATCTCGATTAACCTCACT 1203
QY 343 SerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspVal 362
DB 1204 TCCCAACTACAGACGCCATGCAACTGAATCCGAGCGCTAGTTTAAAGATCGGCT 1263
QY 363 ValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGly 382
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QY 383 ThrSerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAsp 402
DB 1324 ACTCTTTAAAAAATCTCTTGAT---TTGAAGTTAGSTACGTTAGTATCCCTTAT 1380
QY 403 SerLeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArg 422
DB 1381 TCTTTAGTACTGAATAAAGCGTACTATCCAGCC-----CTAATCTTCT 1428
QY 423 IleAspArgProValValLeuAlaIleSerAspGluSerPheTyGlnAsn--GlyPhe 441
DB 1429 ATCCAAAGATCTCTCTCTAATCTGAGATGAGATTTTATGAAATTTAGAGCTT 1488
QY 442 LeuAsnGluAspHisSerTyAspGlyIleLeuGluLeuAspAlaGlyLysAspIleVal 461
DB 1489 CTCAGTAAAGACAAACAAATATCTCTCTTACTCTCCCTAAAGACAAATCTCATTTA 1548
QY 462 IleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyGlyTyGlnGlyLys 481
DB 1549 CATCTTCTGATGGAAAC-----CTCTCTTCTCACTTGGATATCAAGAGAT 1596
QY 482 TyrThrIleAsnTyPheThrAspAspLys-----LysAlaThrValSerTyrAlaLys 499
DB 1597 TGCACTTTCTTGGAAGATTTCTGTAAGAGCGCATCTCTGATTCCTAATGACGCT 1656
QY 500 GlnSerPheAsnProThrAlaGluGlnAlaProLeuValProAsnLeuLeuTyrGly 519
DB 1657 AAAAATATGTCCTCATCCAGAACGTCATCTACATCGTTGCGAACACTTTTGAAAC 1716
QY 520 SerPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluIlePro 539
DB 1717 ACCTATTCGATATCAAGCTGTGCAATGATGATTAATCAACAGCGCACGAGAGACC 1776
QY 540 TyrGluLysArgPheTyrValAlaGlyIleSerAsnVal-----LeuHisArgSerGly 557
DB 1777 TATCATATTGGAACGTGGAGATCTGCTTTTCTATTTATCTATGATACACAGACTCT 1836
QY 558 ArgGluAsnGlnLysPheArgHisValSerGlyGlyAlaValAlaGlyAlaSerThr 577
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QY 578 ArgMetProGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLys 597
DB 1897 CACAGTTTAGATGACATTTCTTCTGCTTGGCTGACAGACAAATTACTCGGAAATCTGC 1956
QY 598 AspTyPheMetAsnThrAsnPheAlaLysThrTyAlaGlySerLeuArgLeuGlnHis 617
DB 1957 GATTCCTTATTAAGCTACAGAAACGACCTCTATATAGCTACTACAAACGCAATCT 2016
QY 618 AspAlaSerLeuTySerValValSerIleLeuLeuGlyGlyGlyLysArgGluIle 637
DB 2017 GCTACCTCTAATGAATAATCTGCA----- 2043
  
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QY 638 LeuLeuProTyValSerIyThrLeuProCySerPheTyGlyGluLeuSerTyGly 657
 DB 2044 -----CAGGATGCTCAAT 2058
 QY 658 HisThrAspHisArgMetIyThrGluSerLeuProProProThrLeuSerThr 677
 DB 2059 GAAAGTATCCATAGCTAAACAAATAT-----CGCTCTCTCTAA 2103
 QY 678 Asp---HisThrSerTyrGlyIyValTyrValTyrAlaGlyGluLeuGlyThrArgValAla 696
 DB 2104 GAAGATTCGGATTCGGATTCGGATTCGGATTCGGATTCGGATTCGGATTCCT 2163
 QY 697 ValGluAsnThrSerGlyArgGlyPhePheGlnIyValTyrThrProPheValIyValGln 716
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 QY 737 AspSerHisLeuTyrThrLeuAlaIleProLeuGlyIleLeuGlyIyValArgPhe--- 755
 DB 2281 GCCAGCTCTTCAGAAATATTCATCTTCATAGAAATACATTGAAAAATCCCA 2340
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 DB 2578 CTGGGAGCACCTTACAGGTTCT 2598
 RESULT 15
 US-09-556-877-171
 ; Sequence 171, Application US/09556877
 ; Patent No. 6432916
 ; GENERAL INFORMATION:
 ; APPLICANT: Probet, Peter
 ; APPLICANT: Bhactia, Ajay
 ; APPLICANT: Skeiky, Yasir
 ; APPLICANT: Fling, Steve
 ; APPLICANT: Maisonneuve, Jeff
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
 ; FILE REFERENCE: 210121.469C5
 ; CURRENT APPLICATION NUMBER: US/09/556, 877
 ; NUMBER OF SEQ ID NOS: 305
 ; SOFTWARE: FASTSEQ for Windows Version 3.0/4.0
 ; SEQ ID NO 171
 ; LENGTH: 2895
 ; TYPE: DNA
 ; ORGANISM: Chlamydia
 US-09-556-877-171
 Alignment Scores:
 Pred. No.: 1,71e-46 Length: 2895
 Score: 527.50 Matches: 209
 Percent Similarity: 37.54% Conservative: 121
 Best Local Similarity: 23.78% Mismatches: 338
 Query Match: 12.28% Indels: 211

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 US-09-830-446-27 (1-841) x US-09-556-877-171 (1-2895)
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 QY 43 ThrSerPheSerSerIyThrSerAlaThrAspGlyThrAsn----- 57
 DB 517 AAGACCTTTCTTANGTCCAGAGAGGATTAAGTACCGCTTAATCTTTGTTGAGC 576
 QY 58 -----TyrValPheLysAspSerValIleGluAsnValProLysThr 72
 DB 577 GAGATCAGCTTTGTTTCTTTATGACACACATCTGATTTCAACT----- 624
 QY 73 GlyIuThrGlnSerThrSerCysPheLysAsnAspAlaAlaGlyAspLeuAsn 92
 DB 625 -----AATACAGACAGAAAGTGGCGCTATCTAT 654
 QY 93 LeuGlyGlyIyPheSerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAla 112
 DB 655 GCTGGAACGAGCAATTTCTTTGAGAGTAAATCTGCAATCTTCTTCAATCAATTAACGCC 714
 QY 113 AlaIleGlySerGlyAlaAlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSer 132
 DB 715 TGTTCGACAGAGAGCG----- 732
 QY 133 PheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValLysGly 152
 DB 733 ---ATCTTCTCCCTATCTGTTCTTCAACAGAAAT-----CGTGT 771
 QY 153 AsnLeuSerLeuLeuAsnAsp-----LysValLeuIleGlnAsnAsnPheSerThr 170
 DB 772 AACATGTTTCTATTAATGCTGCTTTAAATGAGAAACAGCTTCTTCAAGAGCT 831
 QY 171 GlyAspGlyGlyAlaIleAsnLysAlaGlySerLeuLysIleAlaAsnAsnLysSer--- 189
 DB 832 TCTGATGAGAGCAATTAAGTAACTACTGCTGATGATGATGATGATGATGATGATGATG 891
 QY 190 LeuSerPheIleGlyAsnSerSerThrArgGlyIyAlaIleHisThrLysAsnLeu 209
 DB 892 ATCTTTTATGACAAATATCACAAAATTAATGCGAGATTAATGATGATGATGATGATG 951
 QY 210 ThrLeuSerSerGlyGlyIuThrLeuPheGlnGlyAsnThrAlaProThrAlaAlaGly 229
 DB 952 ACCCTGATGATTAATGCTTACTTATTAATTAAT-----ATCGCAATTAAT 1002
 QY 230 LysGlyGlyAlaIleAlaIleAlaIleAspSerGlyThrLeuSerIleSerGlyAspSerGly 249
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 QY 250 AspIleIlePheGluIyAsnThrIle-----GlyAlaThrGlyThrValSer 265
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 DB 1123 TCAGCTAATCTCTTGAAGAATATGCAATTAATGAGCAAGCTCTGCTGTAATTTCTA 1182
 QY 280 LeuArgAlaAlaGlnIyHisThrIleTyrPheTyrAspProIleThrValThrLysSer 299
 DB 1183 TTGAGAGCGAGAGTACCAAAATTTAATTTTATGATCTTATTAATGTAATGTAATGTA 1239
 QY 300 ThrSerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGlyTyr 319
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 QY 320 ThrGlyThrIleValPheSerGlyIyLysLeuThrGluAlaGlyAlaLysAspGlyLys 339
 DB 1279 ACAGGCTGTGTGATTTTTCAGAGCTACTGTTATTCGAGATTTT---CATCAAGC 1335
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      1396  GATATGCTGACGCTTACAGTAATGATTCACACAACTGGGGGT-----GTGTT 1446
      380  AspleuGlyThrSerIleuVal-----AlaAsn 388
      1447  TCTCTGGGAATGAGCAGTTCTGAGTGTCTATAAAATGATGACAGAGATTCTGCTAC 1506
      389  ThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSer---LeuArgAsnGly 407
      1507  AATGCTCTATAACCTGAGCATATTGGAATTCCTTCTTCATCTGATAAAAGTGT 1566
      408  LysIleValIleLeu-----SerAlaIleThrAlaGlnIleAspIleArgIleAsp 424
      1567  GCTGAGATTCCTTATTTGTGGGTAGAGCTCAAAATACAGCAATACCTATACAGCAGAT 1626
      425  ArgProValValIleuAlaIleSerAsp-----Glu 434
      1627  ACTGACGCTACCTTCTATGATGATGTAATAAATCTCAGTATGATGACTAGAGGAAC 1686
      435  SerPheTyrglnAsnGlyPheLeuAsnGlnAspHisSerTyrglyIleLeuGluLeu 454
      1687  TCTCTTATGATACCAAGATCTGACCCATGCTGTGATCAACAGCCATGCTATCTATT 1746
      455  AspAlaGlyLysAspIleValIleSerAlaAspSerArgSerIleAspAlaValGlnSer 474
      1747  TCTGAAGCTAGCAGTAACCAAGCTACATCAAGAAATATAGATTTTCGGACTAAATGTC 1806
      475  Pro---TyrglyTyrglnGlyLysTrpThrIleAsnTrpSer----- 487
      1807  CCTCATATTATGATGCAAGGACTTTTGACTTGGGGCTGGGCAAAAACCAAGATCCAGA 1866
      488  -----ThraspAspLysValAlaThr----- 494
      1867  CCAGCATCTTCAGCAACAATCATCTGATCCACAAAAGCCAAATAGATTTCATAGAACCTTA 1926
      495  ---ValSerTrpAlaLysGlnSerPheAsnProThrAlaGlnGlnIleAlaProLeuVal 513
      1927  CTACTAACATGCTTCCTCCGCGGGATATGTTCTTAGCCCAAAACACAGAAAGTCCCTCATTA 1986
      514  ProAsnLeuLeuTrpGlySer---PheIleAspValArgSerPheGlnAsnPheIleGlu 532
      1987  GCTAACACCTTATGCGGGAAATATGCTGTCGACACAGAAAGCTTAATAAATAGTCAGAG 2046
      533  LeuGlyThrGlnGlyAlaProTyrglyLysArgPheTrp-----ValAlaGlyIle 549
      2047  CTGACACCTAGTGTATCTCT-----TTCTGGGAATTACAGAGAGAGAGACTTA 2094
      550  SerAsnValIleuHisArgSerGlyArgGlnAsnGlnArgLysPheArgHisValSerGly 569
      2095  GGCAATGATGCTTACCAAGATCTCGAAGAAATCATCTGAGTTCCATATGCGCTCTTCC 2154
      570  GlyAlaValAlaGlyAlaSerThrArgMetProGlyGlyAsp-----ThrLeuSerLeu 587
      2155  GGATACTCTGGCGGG-----ATGATAGCAGGGGAGACACACACCTTCTCATTTG 2202
      588  GlyPheAlaGlnLeuPheAlaArgAspLysAspTyrgPheMetAsnThrAsnPheAlaLys 607
      2203  AAATTCAGTCAGACCTCACCAAA-----CTCAATGACGTTTACGCCAAA 2247
      608  ThrTyralaGlySerLeuArgLeuGlnHisAspAlaSerLeuTyrgSerValValSerIle 627
      2248  AACAACTATCTTCT-----AAAATTACTATGCAAGAGAAATGCTCTTC 2295
      628  LeuLeuGlyGlnGlyLysLeuArgGlnIleLeuLeuProTyrgValSerIleThrLeuPro 647
      2296  TCATTGCAAGAAAGTTTCTTGCTGACTAAATAGTT----- 2331
      648  CysSerPheTyrglyGlnLeuSerTyrgly---HisThrAspHisArgMetLysThrGlu 666

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      2380  GGA----- 2382
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      2383  -----GAAATCTAACATCTCAAGGACGTTTC 2409
      707  GlnGlyTrpThr----- 710
      2410  CGCAGTCAAACGATGGAGAGGTGCTGTTTGTATCTCCCTATGAACCTTTGATCA 2469
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      2470  ACGCATATACAGACGCTCCCTTTTAGTGCTCTTGATATTATTTCTAGGCTGTCTCAC 2529
      725  PheValGlnLeuGlyAlaIleSerArgAspPheSer---AspSerHisLeuTyrgAsnLeu 743
      2530  TTTACTGAGGTGGAGGCTATCCCGGAAGCTTTTCTACAAAGACTCTTGATCATATGTC 2589
      744  AlaIleProLeuGlyIleLys-----LeuGluLysArgPheAlaGlnGlnTyrg 760
      2590  CTAGTCCCTATGAGATTAAAGGTAGCTTTATGATGCTTACCAAGCTCAAGCTCAAGCCTGG 2649
      761  HisValValAlaMetTyrgSerProAspValCysArgSerAsnProLysCysThrThr 780
      2650  ACTGTAAATGGCATACCAACCCGTTCTGTATAGACAGAAACCAAGGATGCGACCCAG 2709
      781  LeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsnLeuAlaArgGlnAla 799
      2710  CTCCTAGCCAGTAAGGATATTGTTGTTGTTAGTGAAGCCCTCATGCGCGTATGCC 2766

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Search completed: January 29, 2004, 17:03:03
Job time : 1583 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 29, 2004, 10:21:11 ; Search time 722 Seconds
(without alignments)
4245.252 Million cell updates/sec

Title: US-09-830-446-27
Perfect score: 4235
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Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2434939 seqs, 1822278265 residues
Total number of hits satisfying chosen parameters: 4869878

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -MODE=frame+ .p2n model -DRV=xlh
-MODL=frame+.p2n model -DRV=xlh
-O=/cgn2_1/USPTC_spool/US09830444/runat_29012004_102103_19252/app_query.fasta_1.1031
-DB=Published Applications NA -QMT=faetap -SUFFIX=p2n.tmpb -MINMATCH=0.1
-LOOPL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blomsum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pcp -THR MAX=100
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-LONGLOG -DRV_TIMEOUT=120 -WANT_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Database : Published Applications NA:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Query Match	Length	ID	Description
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1	4295	100.0	2526	12	US-10-312-273-140	Sequence 140, App
2	4255	99.1	1230025	12	US-10-289-762-1	Sequence 1, Appl1
3	1580.5	36.8	3000	13	US-09-428-122-1	Sequence 1, Appl1
4	1497	34.9	2520	13	US-09-738-269-22	Sequence 22, Appl
5	1497	34.9	2520	14	US-10-023-437-22	Sequence 22, Appl
6	1435.5	33.4	2787	12	US-10-312-273-116	Sequence 116, App
7	1415.5	33.0	2793	12	US-10-312-273-96	Sequence 96, Appl
8	1407.5	32.8	2787	12	US-10-312-273-96	Sequence 96, Appl
9	1379.5	32.1	2787	12	US-10-312-273-96	Sequence 96, Appl
c	1365	31.8	1230025	12	US-10-289-762-1	Sequence 14, Appl1
10	1357.5	31.6	2241	12	US-10-312-273-20	Sequence 20, Appl
11	1335.5	31.1	2811	12	US-10-312-273-154	Sequence 154, App
12	1335.5	31.1	3050	9	US-09-452-380-1	Sequence 1, Appl1
13	1335.5	31.1	3050	13	US-10-324-129-1	Sequence 1, Appl1
14	1335.5	31.1	3050	13	US-10-324-129-1	Sequence 1, Appl1
15	1286.5	30.0	2781	13	US-09-738-269-56	Sequence 56, Appl
16	1286.5	30.0	2781	14	US-10-023-437-56	Sequence 56, Appl
17	1279.5	29.8	2808	9	US-09-452-380-2	Sequence 2, Appl1
18	1279.5	29.8	2808	13	US-10-324-129-2	Sequence 2, Appl1
19	1089	25.4	2922	12	US-10-312-273-4	Sequence 4, Appl1
20	1016	23.7	2769	12	US-10-312-273-42	Sequence 42, Appl
21	1011	23.5	2950	9	US-09-865-468-6	Sequence 6, Appl1
22	1002	23.3	4224	9	US-09-841-132-486	Sequence 486, App
23	1002	23.3	4224	12	US-10-312-273-32	Sequence 32, Appl
24	936	21.9	3021	9	US-09-841-132-182	Sequence 182, App
25	936	21.8	2949	9	US-09-841-132-170	Sequence 170, App
26	828.5	19.3	2040	13	US-09-738-269-52	Sequence 52, Appl
27	828.5	19.3	2040	14	US-10-023-437-52	Sequence 52, Appl
28	711.5	16.6	2643	9	US-09-841-132-169	Sequence 169, App
29	696.5	16.2	2601	9	US-09-841-132-181	Sequence 181, App
30	648	15.1	1065	12	US-10-312-273-16	Sequence 16, App
31	559	13.0	1485	12	US-10-312-273-134	Sequence 134, App
32	557	13.0	1745	9	US-09-865-468-10	Sequence 10, Appl
33	555	12.9	1545	12	US-10-312-273-52	Sequence 52, Appl
34	548.5	12.8	1188	12	US-10-312-273-22	Sequence 22, Appl
35	536.5	12.5	5172	9	US-09-841-132-374	Sequence 374, App
36	536.5	12.5	5172	9	US-09-841-132-375	Sequence 375, App
37	536.5	12.5	5172	12	US-10-312-273-120	Sequence 120, App
38	527.5	12.3	2895	9	US-09-841-132-171	Sequence 171, App
39	527.5	12.3	2934	9	US-09-841-132-183	Sequence 183, App
40	509.5	11.9	3050	10	US-09-779-081-1	Sequence 1, Appl1
41	509.5	11.9	4830	12	US-10-312-273-84	Sequence 84, Appl
42	509.5	11.9	4830	13	US-09-841-260-59	Sequence 59, Appl
43	509.5	11.9	4830	14	US-10-007-693-59	Sequence 59, Appl
44	506	11.8	5265	9	US-09-841-132-174	Sequence 174, App
45	502	11.7	5253	9	US-09-841-132-421	Sequence 421, App

ALIGNMENTS

RESULT 1
US-10-312-273-140
Sequence 140, Application US/10312273
Publication No. US2004000567A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
FILE REFERENCE: P025035MO
CURRENT APPLICATION NUMBER: US/10/312,273
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 0016363.4
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 0017047.2
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 0017983.8
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: 0019368.0
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: 0020440.4
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: 0022583.9
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 0027549.5
PRIOR FILING DATE: 2000-11-10

PRIOR APPLICATION NUMBER: 0031706.5
 PRIOR FILING DATE: 2000-12-22
 NUMBER OF SEQ ID NOS: 664
 SOFTWARE: Seqwln99, version 1.02
 SEQ ID NO 140
 LENGTH: 2526
 TYPE: DNA

ORGANISM: Chlamydia pneumoniae
 US-10-312-273-140

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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US-09-830-446-27 (1-841) x US-10-312-273-140 (1-2526)

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DB 241 TTTAAATAATGACGCTGACGCTGAGATCTAAATTTCTTAGAGGGGGAATTTCTTTTACA 300
QY 101 PheSerAsnIleAspAlaThrlThrlAsnSerGlyAlaIleGlySerGluAlaAsn 120
DB 301 TTTAGCAATATGATGATGACCAACAGCGCTTCGAGCTGATAGGAAGTGAACAGCTAAT 360
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DB 421 GTGACTATAGATTTGGAGCTTATCAATGTTAAAGGAATTTAAAGCTTATGATTAATGAT 480
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DB 781 ACAGGAACCGTCTCTCATATGCTATTGATTAGAACTAGCGCTAAGATACGCGTTA 840
QY 281 ArgAlaIleGlnGlyHleThrlIleTyPheTyTrsProlleThrlValThrlGlySerThr 300
DB 841 CGTCTCGCGCAAGAGACATACATATCTTTATATATCGATTAATCTGTAACGAGATTCACA 900
QY 301 SerValAlaAspAlaLeuAsnIleAsnSerProAspThrlGlyAspAsnLysGlyTyTrsThr 320
DB 901 TCTGTGCTGATGCTCTCATATATTAATAGCCCTGATCTGAGATTAACAAAGATTAACG 960
QY 321 GlyThrlIleValPheSerGlyGlyLysLeuThrlGluAlaGlyAlaLysAspGlyLysAsn 340
DB 961 GGAACCATAGCTTTCTTCGAGAGAGCTGACGAGGACAGAACTTAAAGAGAGAGAAC 1020
QY 341 ArgThrlSerLysLeuLeuGlnAsnValAlaPheLYsAsnGlyThrlValIleLeuLysGly 360
DB 1021 CGCACTTCTAAATTAATTCAAAATGTTGCTTTTAAATGAGGAGCTGATGTTTAAAGGT 1080
QY 361 AspValIleLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAsp 380
DB 1081 GATGTCGTTTAAATTCGGAACGCTTTCTCTCAGATGCAAACTTAAGTTGATTAATGAT 1140
QY 381 LeuGlyThrlSerleuValAlaAsnThrlGluSerIleGluLeuThrlAsnLeuGluIleAsn 400
DB 1141 TTAGGAGAGCTGTTGTTGTTGCAACACCGAAAGTATCCAGATTAACGAATTTGAAATTAAT 1200
QY 401 IleAspSerLeuAsnGlnGlyLysIleLysLeuSerAlaAlaThrlAlaGlnLysAsp 420
DB 1201 ATTAACCTCTTCAGAAACAGGAAAGATTAACCTAGTGTGTCACAGCTCACAAGAGAT 1260
QY 421 IleArgIleAspAspProValIleuAlaIleSerAspGluSerPheTyGlnAsnGly 440
DB 1261 ATTGCTATAGATCGTCTGTTGCTGATCTGCAATTAAGCATAGAGATTTTATCAAAATGCG 1320
QY 441 PheLeuAsnGluAspHleSerTyTrsAspGlyIleLeuGluLeuAspAlaGlyLysAspIle 460
DB 1321 TTTTGAATAGAGACCAATCTCTATGATGAGATTCCTTAGATGATGCTGGGAAAGACATC 1380
QY 461 ValIleSerAlaAspSerArgSerIleAspAlaValAlaGlnSerProTyTrsGlnGly 480
DB 1381 GTGATTTCTGCAAGATTCCTCGAGATATAGATGCTGTACATCTCGTATGAGCTATCAGGGA 1440
QY 481 LysTrpThrlIleAsnTrpSerThrlAspAspLysIleValAlaThrlValSerTrpAlaLysGln 500
DB 1441 AAGTGAACATCAATTTGCTCTACATGATATAGAAAGCTACGGTTTCTTGGGCGAAGAG 1500
QY 501 SerPheAsnProThrlAlaGluGlnLysAlaProleuValProAsnLeuLeuTrpGlySer 520
DB 1501 AGTTTAAATCCACATGCTGACAGAGAGGCTCGTTAGTTCTTAATCTTCTTGGGGTCT 1560
QY 521 PheIleAspValArgSerPheGlnAsnPhelIleGluLeuGlyThrlGluGlyAlaProTyTrs 540
DB 1561 TTTATAGATGTTGCTCTCTTCAGAAATTTTATAGCTAGTACTGAAAGGTGCTCTTAC 1620
QY 541 GlyLYsAspPheTrpValAlaGlyIleSerAsnValLeuHleArgSerGlyArgGluAsn 560
DB 1621 CAAGAAGATTTTGGGTTGAGGCAATTTCCATATGTTTGCATAGAGAGGCTCGTAATAAT 1680
QY 561 GlnArgLysPheArgHleValSerGlyGlyAlaValAlaGlyAlaSerThrlArgLysPro 580
DB 1681 CAAGAAGATTTCCGTCATGTCAGTGAAGTCTGTAGTGAAGTGTGTCAGACAGAGATGCGG 1740
QY 581 GlyGlyAspThrlLeuSerLeuGlyPheAlaLeuPheAlaArgAspLysAspTyTrsPhe 600
DB 1741 GGTGTATATACCTGCTCTGAGTTTGTCTCAGCTCTTTCGCGGACAAAGACTACTTT 1800
QY 601 MetAsnThrlAsnPhelAlaLysThrlTyTrsAlaGlySerLeuArgLeuGlnHleAspAlaSer 620
DB 1801 ATGAATACCAATTTCCGAAAGACCTACGAGATCTTTACGTTTGCACAGATGCTTCC 1860
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NAME/KEY: misc feature
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OTHER INFORMATION: n=a or c or g or t
FEATURE:

Alignment Scores:
Pred. No.: 0 Length: 1230025
Score: 4255.00 Matches: 840
Percent Similarity: 99.76% Conservative: 0
Best Local Similarity: 99.76% Mismatches: 1
Query Match: 99.07% Indels: 2
DB: 12 Gaps: 0

US-09-830-446-27 (1-841) x US-10-289-762-1 (1-1230025)

QY 1 MetLySIIeProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAa 20
Db 28950 ATGAAGATTCACCTCGCTTTTATTGATATCATTAAGTACCAAGCTTCTATGCGAAT 29009

QY 21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAaSerPheAspGlyThrThr 40
Db 29010 TTATTAGGAGCTGCTACTACCAAGAGTTATCGCTAGCAATAGCTTCATGAACTACA 29069

QY 41 SerThrThrSerPheSerSerIleThrSerSerAlaThrAspGlyThrAsnTyrrValPhe 60
Db 29070 TCACACACAGCTTTTCTAGTAAACATCATCGCTACAGATGACCAATTAATGTTTTT 29129

QY 61 LysAspSerValValIleGluAsnValProLysThrGlyIleThrGlnSerThrSerCys 80
Db 29130 AAAAGATTCTGATGTTATGAAAAATGATACCAAAACAGGGGAACTCAGTCTACTAGTTCT 29189

QY 81 PheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyPheSerPheThr 100
Db 29190 TTTAAAAATGACGCTGACGCTGAGATCTAAATTTCTTAGAGGGGGATTTTCTTTCACA 29249

QY 101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAsn 120
Db 29250 TTTAGCAATATCGATGCAACCAACGCTTGTGAGCTGCTAATTGGAAGTAAACAGCTAAT 29309

QY 121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
Db 29310 AAGACAGTCACGTTATCAGAGATTTTCGGCACTTCTTTCTTAATCCCAAGCAAGTACA 29369

QY 141 ValThrAsnGlyLeuGlyAlaAlaIleAsnValLysGlyAsnLeuSerLeuAspAsnSer 160
Db 29370 GTGACTAATGAGATTGGAGCTATCAATGTTAAAGGAAATTTAAGCTTATGATATATGAT 29429

QY 161 LysValLeuIleGluAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly 180

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Db 29430 AAGGTATGATTGAGACAAATTTCTCAACGAGATGGCGACA-ATTATTTGCGAGGC 29488
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Db 29489 TCTTTGAAGATCGCAACAAATTAAGTCCCTTTTATTTGAAATAGTTCTTCAACCGT 29548
Qy 201 Gly1yAla1Le1eH1eThrLyAenLeuThrLeuSerSerG1yG1uThrLeuPheG1n 220
Db 29549 GGGGAGGCGATTATCCAAAACCTCACTATCTTCTGTTGGGAAACTCATTTTCAG 29608
Qy 221 GlyAenThra1aProThra1aAlaG1yLyG1yAla1Lea1Lea1aAenSerG1y 240
Db 29609 GGGAAATACAGCGCTCAACGCTGCTGTAAGAGAGTCTATCCGATTGCAAGACTCGGC 29668
Qy 241 ThrLeuSer1LeuSerG1yaAenSerG1yaAen1Lea1ePheG1uG1yaAenThr11eG1yAla 260
Db 29669 ACCCTATTCATTTCTGAGACAGTGGGACATTAATCTTTGAAGGCAATACAGATGAGAGCT 29728
Qy 261 ThrG1yThra1aSer1aSer1a1LeaAenG1yThraSer1aLyS1eThra1aLeu 280
Db 29729 ACAAGAACCGTCTCTCACTAGTGTCTATTAGGAATAGCGCTAAGATTAATCTGCTTA 29788
Qy 281 ArgAlaAlaG1nG1yH1eThr11eTyPheTyAenPro11eThra1ThrG1ySerThr 300
Db 29789 CGGCTGCGGACAGACATACGATATCTTTATGATCCGATTCTGTAACAGATCGACA 29848
Qy 301 SerVal1aAenPalaAen1LeaAenSerProAenThrG1yaAenLyS1eThra1aLeu 320
Db 29849 TCTGTTGCTGATGCTCTCAATATTAATAGCCCTGATATCTGAGATTAACAAAGATATACG 29908
Qy 321 GlyThr11eValaPheSerG1yG1uLyS1eThrG1uAlaG1uAlaLyAenPalaAen 340
Db 29909 GGAACCATAGTCTTTCTTGGAGAGAGCTCAACGAGGCAAGACTAAGATTAAGAGAGAAC 29968
Qy 341 ArgThSerLyS1eLeuG1naAenVala1aPheLyAenG1yThraVala1eLeu-LyS1e 360
Db 29969 CGACATCTCAATTAATTAATCAAAATGTTGCTTTAAAATGGGACTGTAAGTTTGAAGAACG 30028
Qy 360 yAenPala1aLeuSer1aAenG1yPheSerG1naAenPalaAenSerLyS1eLeu1eMetas 380
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Qy 380 PLeuG1yThSerLeuVala1aAenThrG1uSer11eG1uLeuThraAenLeuG1u1eas 400
Db 30089 TTTAGGAGCGTCTGTTGTTCCAAACCGAAAGATGAGATTAAAGAAATTTAA 30148
Qy 400 n1LeaAenSerLeuArgAenG1yLyLyS1eLyS1eLeuSer1aAlaThra1aG1uLyS1e 420
Db 30149 TATAGACTCTCTCAAGAACGGAATAAAAGTCAAGTGTGCCACAGCTCAGAAAGA 30208
Qy 420 P1LeaG1y1LeaAenPalaAen1Vala1eLeuA1a1LeaSerPalaAenPalaAenG1 440
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Qy 440 yPheLeuAenG1uAenP1aSerTyAenPala1eLeuG1uLeuAenPala1aG1yLyS1e 460
Db 30269 CTTTGAAGAGAGACATTCCTATGATGAGATTTCTGAGTTAGATGCTGGAAAGACAT 30328
Qy 460 eVal11eSer1aAenPalaAenSer11eAenPala1aG1nSerProTyG1yTyG1nG1 480
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Qy 480 yLyS1eThr11eAenThra1aSerThraAenPala1eThraAenPala1eThraAenPala1e 500
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Qy 500 nSerPheAenProThra1aG1uG1nG1uAlaProLeuVala1ProAenLeuThraPala1e 520
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Db 30509 TTTATAGATGTTGTTCTCTCCAGAAATTTATAGAGCTAGTACTGAAGTCTCTTA 30568
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Db 30569 CGAAAGAGATTTTGGGTTGCGAGGCAATTTTCCATGTTTTCATAGAGCGGTCGTAAAA 30628
Qy 560 nG1naArgLyS1eAenArg1eValaSerG1yAlaVala1aG1yAlaSerThraAenPala1e 580
Db 30629 TCABAAGAAATTCGCTCATGTAGTGAAGTGTGTATAGATGCTAGACAGAGATGACC 30688
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Qy 620 rLeuTySerVala1aSer11eLeuLeuG1yG1uG1yG1yLeuAenG1u11eLeuAenPala1e 640
Db 30809 CCTATACTGTTGATGATGATCTTTTAAAGAGAGAGAGACTCCGAGATCTGTTGCC 30868
Qy 640 cTyTyA1aSerLyS1eThraPala1eProCyS1eThraPala1eThraPala1eThraPala1e 660
Db 30869 TTAATGTTTCCAGACTCTGCGGCTCTTCTTAATGAGGAGCTTAAGCTAGCGCATAGCA 30928
Qy 660 pHisArgMetLyS1eThra1aSerLeuProProProProProProThraPala1eThraPala1e 680
Db 30929 TCAATCCATGAAGACCGAGTCTTACCCCCCCCCCCCCCGAGCTTCCAGAGATCATAC 30988
Qy 680 rSerThraPala1eThra1aThra1aThra1aThra1aThra1aThra1aThra1aThra1a 700
Db 30989 TTTCTGGGAGGATATGCTCGGCTGAGAGCTGGAGACTCGAGTTGCTGTTGAAATATAC 31048
Qy 700 rSerG1yAenG1yPhePheG1nG1uTyThraPheAenVala1aVala1yAla1yAla 720
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Qy 740 uTyAenLeuA1a1eProLeuG1y11eLyS1eG1uLyS1eAenPala1eG1uG1nTyTy 760
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Qy 760 rHisVala1a1aMetTySerProAenPala1eCyAenSerAenPala1eCyAenThra1a 780
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Qy 780 rLeuLeuSerAenG1nG1ySerThraPala1eThraPala1eThraPala1eThraPala1e 800
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Db 31409 TGGCTTTGATGAGCGGAGATTTCTCTGATGATTAATGATAGCGGATGAGCAAAATCA 31468
Qy 840 sPhe 841
Db 31469 ATTT 31472

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RESULT 3

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US-09-428-122-1
; Sequence 1, Application US/09428122
; Publication NO. US20030170259A1
; GENERAL INFORMATION:
; APPLICANT: Connaught Laboratories Limited
; APPLICANT: Murdin et al.

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TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
 TITLE OF INVENTION: USES THEREOF
 FILE REFERENCE: 19721-007-019
 CURRENT APPLICATION NUMBER: US/09/428,122
 CURRENT FILING DATE: 1999-10-27
 EARLIER APPLICATION NUMBER: 60/106,046
 EARLIER FILING DATE: 1998-10-28
 EARLIER APPLICATION NUMBER: 60/132,271
 EARLIER FILING DATE: 1999-05-03
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
 LENGTH: 3000
 TYPE: DNA
 ORGANISM: Chlamydia pneumoniae
 FEATURES:
 NAME/KEY: CDS
 LOCATION: (101)..(2884)
 US-09-428-122-1

Alignment Scores:
 Pred. No.: 1,086-151 Length: 3000
 Score: 1580.50 Matches: 375
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 Best Local Similarity: 39.72% Mismatches: 306
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US-09-830-446-27 (1-841) x US-09-428-122-1 (1-3000)

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 154 LeuSerLeuLeuAspAsnAspLyValLeuIleGlnAspAsnPheSerThrGlyAspGly 173
 545 TTGAATTGGACAAAATAATGTCTAGTTGCTTTCAGCAAAAACCTTTCAACGATATGCG 604
 174 GlyAlaIleAsnCyS----- 178
 605 GGTGCTATACCGCAAAAACCTTTCTATTACAGGAGCTACAAATGCTAGCTCTGTTTCT 664
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 178 ----- 178
 725 GAAACCAAGGGAAGTCTTTTCTGACAAATCTTTCGAAATTCGAGACTGCAATT 784

179 -----AlaGlySerLeuLyIleAlaAsnAsnLySerLeuSerPheIle----- 193
 785 TTTACAGAAAGCTCGGAGACTATTCTTAATATCTAAAGTTCTTATTAGACATTAAG 844
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 194 -----Gly 194
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 965 AATACATGACACACAGCGGAGAGCTATCTATGAAAAGGCTCGAAGCTGCTCCGGA 1024
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 230 LyGlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSerGly 249
 1073 AAAGTGAAGCATAGCTATGAAAGATAGTGGAAATGAGTTATCCGCCGATAGTGT 1132
 250 AspIleIlePheGluGlyAsnThrIleGlyAlaThr-----GlyThrValSerHisSer 267
 1133 GACATTTGCTTTTAGGGAATACAGTCACTCTACTCTCTGAGAGC---AATAGAAAT 1189
 268 AlaIleAspLeuGlyThrSerAlaLyIleThrAlaLeuArgAlaAlaGlnGlyHisThr 287
 1190 AGTATCGACTTAGGAACAGAGTCAAAAGTACACCTTGTGCTGCTGAGTAGAGCC 1249
 288 IleTyrrPheTyrrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsn 307
 1250 ATCTACTTCTATGATCCCATATCACTACAGATCATCCACACAGTTACAGATGCTTAA 1309
 308 IleAsnSerProAspThrGlyAspAsnLyGluTyrrThrGlyThrIleValPheSerGly 327
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 328 GlnLyLeuThrGluAlaGluAlaLyAspGlyLyAsnAsnTyrrSerLyLeuLeuGln 347
 1370 GAAAGTTATCAGAGACAGAGCGCAGATCTTAAATCTTACTTCAAACTACTACAG 1429
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 1430 CCGTAACTCTTTCAGAGAGTACTCTATCTTAAACATGAGAGTACTCTCAGACTCAG 1489
 368 GlyPheSerGlnAspAlaAsnSerLyLeuIleMetAspLeuGlyThrSerLeu---Val 386
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 387 AlaAsnThrGlnSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuAsn 406
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 1604 GCAAAAGAGGCAAAAATGAAACCAAGCTACGCAAAAATCTGACTTATCTGGAACC 1663
 427 ValIleLeuAlaIleSerAspGlySerPheTyrrGlnAsnGlyPheLeuAsnGluAspHis 446
 1664 ATCACTTATTAGAACCGGACGCGCATTTATGAAAATCATAGTTTAAAGAAATCTCAG 1723
 447 SerTyrrAspGlyIleLeuGluLeuAspAlaGlyLyAspIleValIleSerAla---Asp 466
 1724 TCTTACAGAC---ATCTTACAGCTCAAGCTCTGAACTGACCAAGCAGCAGTGA 1780
 466 eArgSerIleAspAlaValGlnSerPro-TyrrGlyTyrrGlnGlyLySerPro---ThrIle 484
 1781 CAGATCTCTAATATGCGTGAAGAAATTCATTAACGCTATACAGGAACTTGGGCGCCAAAT 1840

[illegible]

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Db      2879  CAATTC 2884      :|||
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US-09-738-269-22
; Sequence 22, Application US/09738269
; Publication No. US20030185648A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSTON, STEPHEN A.
; APPLICANT: STEWKE-HALE, KATHERINE
; APPLICANT: SYKES, KATHRYN F.
; APPLICANT: KALTBROECK, BERNHARD
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
; TITLE OF INVENTION: NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
; TITLE OF INVENTION: CHLAMYDIA PSITTACI
; FILE REFERENCE: UTSID:659
; CURRENT APPLICATION NUMBER: US/09/738,269
; CURRENT FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patencin Ver. 2.1
; SEQ ID NO 22
; LENGTH: 2520
; TYPE: DNA
; ORGANISM: Chlamydia psittaci
US-09-738-269-22

Alignment Scores:
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Score:          1497.00      Matches:      357
Percent Similarity: 56.21%      Conservative: 132
Best Local Similarity: 41.03%      Mismatches: 121
Query Match:      34.85%      Indels:      60
Db:                13          Gaps:          25

US-09-830-446-27 (1-841) x US-09-738-269-22 (1-2520)

QY      1      MetlyslleProlenArpHeleuleuilleserLeuValProThrlenserMetSerAen 20
DB      1      ATGAAACATCCAGTCTACTGCTTCTTAATATCC-----TCGACCTATTGGCTCGAAT 54
      |||
QY      21      LeuenglYalAalThrThrluglu-----LeuserAlaSerasnSerPheapgly 38
DB      55      TCTTTGACCTTCGCTTAACGACGCTCAACAGCCTTAACCTCCCTCCGATGCTTAATGGA 114
      |||
QY      39      ThrThrSerThrThrSerSerSerSerlyThrSerSerAlaThrAspGlyThrAenly 58
DB      115      AATGACCTCTGAGGAGATTCGAGTAAAGAACTTATCA-----GGAACAAGTAT 168
      |||
QY      59      ValPheLyasPserValValIleGlubAnValProlysrThrlglYluthrlInserThr 78
DB      169      ACTTGTCGAAACCAATGTGTATCTCCCTTTCGACGGAAAGATTCAGTCAAGTAAAGAAA--- 225
      |||
QY      79      SerCySPheLyasAenAAspAlaIalAglAspLeuAenPheleuglyYglYglPheSer 98
DB      226      AGTGTTC-----TCAGCTACTGATTAACCTTACTTCTTAAGAAACGGGTACT 276
      |||
QY      99      PheThrPheSerAenIleAspAlaThrThrlAserGlyAlaAlaIleGlyserGluAla 118
DB      277      CTTTGCTTGAATATTAATTACTACACAGTACGAGTAAACCCCGAGCATTATATGTTCAAGG 336
      |||
QY      119      AlaAenlysrThrValThrlenserGlyPheSerAlaLeuSerPheleulysrProAla 138
DB      337      CAAGGAAACCACTTACGACATCTCAAGATTTTCTTATTTTCAATGCTTATGTCTCTCA 396
      |||
QY      139      SerThrValThrAenGlyleuglyAlaIleAenVallyGlyAsnLeuSerleuLeuAap 158
DB      397      GGC-----ACAACTGCTTACGACACTATACAGACTTAAAGGCAACAACCTTAAAGAT 450
      |||
QY      159      AenAspLyValleuIleGlnAspAenPheSerThrGlyAspGlyYglYalAlaIleAenCy 178
DB      451      AACTCTAGCTCTGTCTTCCATATAAAACGTCTCAACAGCAAGAGTGGGGCTATCCAGTGT 510
      |||
QY      179      AlaGlySer-----LeuylleAlaAenAenlySerleuSerPheIleGly 194

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Db      511 AAAGAGACAGTGAAGCTGAATTAATAATAGAAATTAATCAGAAATCTGTTTTCAGAA 570
Oy      195 AenSerSerThrArgGlyValIleHisThrIleuHisLeuThrLeuSerSerGly 214
Db      571 AACTCTCTCACTTCAAAAGCGGAGCTATTATAGCTGATTAATCACTAACATGCTCAGCT 630
Oy      215 GlyIuThrLeuPheGlnGlyValSerThrAlaProThrAlaIleGly---LysGlyValIle 233
Db      631 GGGCTACATATTATTCTAACAACTCTGATCCAAAGGTTATCCCTTAAGGCGAGACT 690
Oy      234 IleAlaIleAlaSer---SerGlyThrLeuSerIleSerGlyAspSerGlyAspIleIle 252
Db      691 ATTGACATTAAGATTCAAGTGTGATGATGCTTAACCGCTGATCTCGAGATTATCC 750
Oy      253 PheGlnGlyAsn-----ThrIleGlyAlaThrGlyThrValSerHisSerAla 268
Db      751 TTCATGGAAACCAAAATCATCAAACTAGTGTGAGAGTTCTACGTAAACAGAAATATCC 810
Oy      269 IleAspLeuGlyThrSerAlaIleThrAlaLeuAlaGlnGlyValIleThrIle 288
Db      811 ATAGATCTCGGACA---GGGAAATTACAAAGCTACGCTTAAGAGCGCTTCGAGATT 867
Oy      289 TyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsnIle 308
Db      868 TTCCTCATAGACCTTATTACTGGGGGAGAGATCT-----GATGAATCAAAACAT 915
Oy      309 AsnSerProAspThrGlyAspAsnIleGlyIuThrGlyThrIleValPheSerGlyIu 328
Db      916 AATTAATAAGAAACCTGTGAT-----TATACAGAAAGATGCTTCTTCAGGTAA 966
Oy      329 LysLeuThrGlnAlaGlnAlaIleValAspGlyIuValAsnArgThrSerIleLeuGlnAsn 348
Db      967 AATATTACCGATGAAGAAAGAAAGCAGAGCGAAACCTAGCTTCACTTCAACCAACC 1026
Oy      349 ValAlaIleValAsnGlyThrValValLeuGlyValAspValValLeuSerAlaAsnGly 368
Db      1027 ATCATTATATCAGCAGAGATCTCTTACTTAAGATGATGTAATCTGAACCGCAAAACA 1086
Oy      369 PheSerGlnAspAlaAsnSerIleLeuIleMetAspLeuGlyThrSerLeu----- 385
Db      1087 GTAAAGCAGAAAGCGGATCTACCGTTGATGATCTAGAGCAACATTCACAGCGCT 1146
Oy      386 ValAlaAsnThrGlnSerIleGlyLeuThrAsnLeuGlnIleAsnIleAspSerLeuArg 405
Db      1147 TCTTCAGGTGAGAAACATCACTTAATCTATAGATTTAAATTAATGCGCTCGTTGGGG 1206
Oy      406 AsnGly-----LysIleValIleValSerAlaAlaThrAlaGlnIleValAspIleArg 422
Db      1207 GGGGGGGGGGATCTCTCTGCTAACTCCGCAACAAATACAGCAAGTCAAGCTATACT 1266
Oy      423 IleAspArgProValValLeuAlaIleSerAspGlyIuSerPheTyrGlnAsnGlyPheIleu 442
Db      1267 ATTAAAC---GCTGTAACTAGTCAATGCTGATGAGCAATGCTTAAGAAATCTTAATCTT 1323
Oy      443 AsnGlnAspHisSerTyrAspGlyIleLeuGlnLeuAspAlaGlyValAspIleValIle 462
Db      1324 GCTACGTAAACCTTTCACAGCATATGATGATCACTAACGCTAGTACAGTCAACAG 1383
Oy      463 SerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGlyValTyr 482
Db      1384 CCTACAGATTAATCTAAACAAATTAATGCTCTCACTACATTAAGGTTACCAAGAAATGG 1443
Oy      483 ThrIleAsnTyrSerThrAsp-----AspIleValIleThrValSerThrAlaIleVal 500
Db      1444 ACAGTAACCTTGGAGACAGAAACAGCTACAAACAGCAACCTTAACCTTGGAGAAACT 1503
Oy      501 SerPheAsnProThrAlaGlnGlnIleAlaProLeuValProAsnLeuLeuTyrPheSer 520
Db      1504 GGCTACTCCCTTAACCAAGAGCTTAAAGAGCTTTAAAGTCCGAATACCTTTGGGGTCA 1563
Oy      521 PheIleAspValArgSerPheGlnAsnPheIleGlyLeuGlyThrGlnGlyAlaProTyr 540

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Db      1564 TTCTTGACCTCAGAGCTATACAAACTTAATGATATTAAGCTGAATGGCGTCACTAC 1623
Oy      541 GlnIuValArgPheThrValAlaGlyIleSerAsnValLeuHisArgSerGlyArgIuAsn 560
Db      1524 CATAGAGCTTTTGGGATTCGGGTCTAGCTTACTTTTACCAAAAGTGGCTGATACT 1683
Oy      561 GlnArgIuValPheArgHisValSerGlyValAlaValAlaGlyAlaSerThrArgMetPro 580
Db      1684 AAACGCAAGTCCGTCACAAATAGCGCGGATACCTTTAAGCGCTACGCAAAATCTCT 1743
Oy      581 GlyIuValSerThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspIleAspTyrPhe 600
Db      1744 TCTGATATATTTTCAATGCGGCTTCTGCGCACTCTTGGAAAGACAAAGACTATTTA 1803
Oy      601 MetAsnThrAsnPheAlaIleThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSer 620
Db      1804 GTTCGAAACCAACGCAACATTTACGAGGTTCTCTTATTAATCAGAT--ATCTCC 1860
Oy      621 LeuTyrSerValValSerIleLeuLeuGlyGlyIuValLeuArgGlnIleLeuLeuPro 640
Db      1861 TATTGAGC-----GCTTGGCAAGATCTGCTACAAAC 1893
Oy      641 TyrValSerIuThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAsp 660
Db      1894 ACTATCGGTGAGAGCTCGTTAGTCTTAACGACAGATTAACTTATGTCAGTCTCA 1953
Oy      661 HisArgMetIuThrGln-----SerLeuProProProProThrLeuSerThr 677
Db      1954 AACGACATGAACCAACATGACAGACATTAACGCTCTCTGTAACCAACATGACAGAA 2013
Oy      678 AspHisThrSerTyrGlyIuThrValIleAlaGlyIuLeuGlyThrArgValAlaVal 697
Db      2014 ATCAAGGGATGTTGGGTAACGATGTTTGGAGTCAAGCTGTGCAACTGCTCATC 2073
Oy      698 GlnAsnThrSerGlyArgGlyPhePheGlnGlyIuThrProPheValValGlnAla 717
Db      2074 CAACAGAAATCTTCTC---CTATTCGATATGATACACCTTCTCGAACTTCACTT 2130
Oy      718 ValTyrAlaArgGlnAspSerPheValGlyIuLeuGlyAla---IleSerArgAspPheSer 736
Db      2131 GTGCATACGACCAAGATGATTTAAGAAACATAGCGATCAGGAAGTACTTGAA 2190
Oy      737 AspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleIuValSerGlyIuValArgPheAla 756
Db      2191 AGCAGCATCTCAACCACTTCTGCTATGCGATCAAGTTGAG---AGATTGGCT 2247
Oy      757 GlnGln-----TyrTyrHisValValAlaMetTyrSerProAspValCysArgSer 773
Db      2248 AACCAAGATACAGCTCTTATCATGTCACGCTGCTTAATCTCTGATATGTAAGAGT 2307
Oy      774 AsnProIuValSerThrThrThrLeuLeuSerAsnGlnGlySer-----TyrIuThrIle 791
Db      2308 AACCTGATCTGATCTCTCTGTTAGTAGCCCCCACTGCTGCTGGTAAACGAA 2367
Oy      792 GlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGly 811
Db      2368 GCCAACAACCTTGGCGAAGCGCTTCAATGCTAACAGAGAAACTTCTTTAAGT 2427
Oy      812 AlaAlaIleGlnLeuPheGlyAsnPheGlyPheGlnTyrArgIuValSerArgSerTyr 831
Db      2428 CACAACAATAGAAATCTTACAGCACTTGGTTCCAGCTCAAGGGATCTTCAAGAACTAT 2487
Oy      832 AsnValAspAlaGlySerIleIleValPhe 841
Db      2488 AACGTAGTCTCGAGATGAGATCAAGTTC 2517

```

RESULT 5

US-10-023-437-22

; Sequence 22, Application US/10023437

; Publication No. US20020183272A1

; GENEAL INFORMATION:

; APPLICANT: JOHNSTON, STEPHEN A.

; APPLICANT: STEMBER-HALE, KATHERINE

APPLICANT: SYKES, KATHRYN F.
 APPLICANT: KALTENBOECK, BERNHARD
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING NUCLEIC ACID
 TITLE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
 FILE REFERENCE: US/09-830-446-27
 CURRENT APPLICATION NUMBER: US/10/023,437
 CURRENT FILING DATE: 2001-12-17
 PRIOR APPLICATION NUMBER: 60/225,839
 PRIOR FILING DATE: 2000-12-15
 NUMBER OF SEQ ID NOS: 69
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 22
 LENGTH: 2520
 TYPE: DNA
 ORGANISM: Chlamydia petfecti
 US-10-023-437-22

Alignment Scores:
 Pred. No.: 3,15e-143 Length: 2520
 Score: 1497.00 Matches: 357
 Percent Similarity: 56.21% Conservative: 132
 Best Local Similarity: 41.03% Mismatches: 321
 Query Match: 34,854 Indels: 60
 DB: 14 Gaps: 25

US-09-830-446-27 (1-841) x US-10-023-437-22 (1-2520)

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QY      1 MetLyIleProLeuArghLeuLeuIleSerLeuValProThrLeuSerMetSerAa 20
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      1 ATGAAACATCGAGTCTGATGCTTAAATATCC-----TCGAGCTATTGGCTCGAAT 54

QY      21 LeuLeuGlyAlaAlaThrThrGluGlu-----LeuSerAlaSerAaSerPheAsgly 38
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      55 TCTTTAGAGCTGCTAACAAGCTCAACGCTTAACTCCCTCCCATAGCTTATATGA 114

QY      39 ThrThrSerThrThrSerPheSerSerLyThrSerSerAlaThrAaspGlyThrAeny 58
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      115 AATGTGACCTCGAGAGGTTCCAGTAAAGAACTTCATCA-----GGAACACGTAT 168

QY      59 ValPheLyAaspSerValIleGluAaenValProLyThrGlyLuhThrGlnSerThr 78
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      169 ACTGTGAAAGGCAATGTGTATCTCTTGCAGGAAAGATTCAAGTCTTAAAGAA--- 225

QY      79 SerCyPheLyAaenAaspAlaAlaAlaGlyAaspLeuAaenPheLeuGlyGlyPheSer 98
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      226 AGTGTGTTCT-----TCAGTACTGATTAACCTTACCTTACGAAACGGGTATCT 276

QY      99 PheThrPheSerAaenIleAaspAlaThrAlaSerGlyAlaAlaIleGlySerGluAla 118
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      277 CTGTGCTTGATTAATTAATACTACTACAGCTAGTAACCCGAGCATTAATGTTCAAGT 336

QY      119 AlaAaenLyThrValThriLeuSerGlyPheSerAlaLeuSerPheLeuLySerProAla 138
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      337 CAAGGAAACCTTAGCAATCTCAGAGATTTCTTAAATTTTCATGTCCTTATGTCCTCA 396

QY      139 SerThrValThrAaenLyLeuGlyAlaIleAaenValIleGlyAaenLeuSerLeuAaP 158
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      397 GGC-----ACACTGATCTGTCTTCAATAAAACCTGCTCAACGAGAGGTGGGCTAT 450

QY      159 AaenAaspLyValLeuIleGlnAaenPheSerThrGlyAaspGlyGlyAlaIleAaenCy 178
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      451 AACTGATGCTGTCTTCAATAAAACCTGCTCAACGAGAGGTGGGCTATTCAGTGT 510

QY      179 AlaGlySer-----LeuLyAlaIleAaenAaenLySerLeuSerPheIleGly 194
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      511 AAAGAGAGAGTGTCTGATTAATAAAATGAATAATCAGATCTGCTTCTCAGAA 570

QY      195 AaenSerSerThrArgGlyAlaIleAaenThrLyAaenLeuThriLeuSerSerGly 214
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      571 AACTCTTCACTTCAAAAGCGGGCTATTTATGCTGATTAACCTCAACATGCTCAAGT 630

QY      215 GlyLuhThrLeuPheGlnGlyAaenThrAlaProThrAlaAlaGly---LyGlyGlyAla 233
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
  
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DB      631 GGGCTACATTAATTTCTTAAACAATCTGTATCAACGATTCATCCCTTAAGCGGAGCT 690

QY      234 IleAlaIleAaP---SerGlyThriLeuSerIleSerGlyAaspSerGlyAaIleIle 252
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      691 ATTAGCATTAAGATTTCAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 750

QY      253 PheGlyAaen-----ThrIleGlyAlaThriGlyThriValSerIleSerAla 268
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      751 TTCGATGGGAAACAAATCATCAAACTAGTGTGGAAGTTTCAAGTAAACAGAAATTC 810

QY      269 IleAaenLyThrSerAlaLyAlaIleAaenValIleGlyAaenLeuSerIle 288
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      811 ATAGATCTCGGACA---GGGAAATTTCAAGCTTACGCTTAAAGACGGCTTCGGAAT 867

QY      289 TyrPheLyAaPProIleThrValThriGlySerThrSerValAlaAaPAlaLeuAaenIle 308
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      868 TTCTCTATAGACCTTATTAATGCGGAGAGATCT-----GATACATTAACATT 915

QY      309 AaenSerProAaPThrGlyAaPaaenLySerGlyThrIleValPheSerGlyGlu 328
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      916 AATTAAGAAAGAAAGCTGTGAT-----TATACAGGAAAGATGCTCTTCAAGTGA 966

QY      329 LybLeuThrGluAlaGluAlaLyAaPgluLyAaenAaPThrSerLybLeuGlnAaen 348
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      967 AATTAATCCGATGAAGAAAGAAAGACAGAGCGGAAACCTAGCTTCACTTCAACCAACC 1026

QY      349 ValAlaPheLyAaenGlyThriValIleuLyGlyAaPValIleuSerAlaAaenGly 368
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      1027 ATCACTATTAATCAAGAGATCTTGTATTAAGATGATGATCTGTAAACCCGAAACAA 1086

QY      369 PheSerGlnAaPAlaAaenSerLybLeuIleMetAaPLeuGlyThriSerLeu----- 385
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      1087 GTAAGCAGGAAAGCGGATCTACCGTTCATGATGATGATGATGATGATGATGATGATGAT 1146

QY      386 ValAlaAaenThrGluSerIleGluLeuThriAaenGluIleAaenIleAaPSerLeuAa 405
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      1147 TCTTCAAGTGAAGAAACCATCACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1206

QY      406 AaenGly-----LybLyIleLybLeuSerAlaAlaThriAlaGlnLybAaPlyAa 422
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      1207 GGGGGGGGGGTAACCTCTCTCTTAACTCGCAACAATACAGCAAGTAACCTTAACT 1266

QY      423 IleAaPArProValIleAaenIleSerAaPgluSerPheThriGlnAaenGlyPheLeu 442
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      1267 ATTAAC---GCTGTCAATCTTACGATGATGATGATGATGATGATGATGATGATGAT 1323

QY      443 AaenGluAaPHeSerLybAaPgluIleGluLeuAaPAlaGlyLybAaPlyIleValIle 462
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      1324 GCTACGCTTAAACCTTCAACAGCAATAGAGCTCACTTAAACGCTAGTACAGTACACAG 1383

QY      463 SerAlaAaPArSerIleAaPAlaValIleGlnSerProLybLybGlnGlyIleYbTrp 482
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      1384 CCTACAGATTAATCAACAAATTAATGCTCTCTACTCATTAAGGTATCCAGAAATATG 1443

QY      483 ThrIleAaenThriSerThriAaP-----AaPlybLybAlaThriValSerThriAlaYbGln 500
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      1444 ACGATTACTGAGCAACCGAAACAGCTTACAAAGCAACGCACTTAACTGGGAAACAACT 1503

QY      501 SerPheAaenProThriAlaGluGlnIleAlaPLeuValProAaenLeuThriGlySer 520
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      1504 GGGTACTCCCTTAAACCCAGAAAGCTCAAGGACCTTATGATCCGAAATATCTTTGGGGTGA 1563

QY      521 PheIleAaPValArgSerPheGlnAaenPheIleGluLeuGlyThriGluGlyAlaProTy 540
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      1564 TTCTGTACCTCAGAGCTTAAACAACTTAAGATATTAAGGCTCAATGCGCTGACATAC 1623

QY      541 GlybAaPArPheThriValAlaGlyIleSerAaenValIleuIleAaPArSerGlyArgGluAa 560
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      1624 CATTAAGATTTTGGGTATCCGCTTACGATTAATCTTACCAAAAGTGGCTGATACT 1683

QY      561 GlnArgLybPheAaPHeIleValSerGlyAlaValAlaGlyAlaSerThriArgMetPro 580
        |||...|||...|||...|||...|||...|||...|||...|||...|||...
DB      1684 AAACCAAGTTCGTCACAAATAGCCCGGATAGCGCTTAAAGCGTCTACGCAAAACTCCT 1743
  
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QY 581 GlyIysAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPhe 600
DB 1744 TGTATGATATTTTCAGTGGCGCTTTCGCCAACTCTTCGAAAGACAAAGACTATTTA 1803
QY 601 MetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuAspGlnHisAspLysSer 620
DB 1804 GTGTGAAAAACCAAGCCCAACATTTACGAGGTTCTCTATATACAGAT---ATCTCC 1860
QY 621 LeuTyrSerValIaSerIleLeuLeuGlyGlnGlyLeuAspGlnIleLeuLeuPro 640
DB 1861 TATTGAGC-----GCTTGGCAAAATCTGCTACAAAC 1893
QY 641 TyrValSerIleThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAsp 660
DB 1894 ACTATCGGAGCAAGCTCCGTTAGCTCTTAACGACAGTTAACTTATGTGATGCTTCA 1953
QY 661 HisArgMetIleThrGln-----SerLeuProProProProProThrLeuSerThr 677
DB 1954 AACGACATGAAAAACCAACATGACGACTACTACGCTCCCTGTAACCAACATGATCAGAA 2013
QY 678 AspHisThrSerTyrGlyTyrValTyrPalaGlyGlnLeuGlyThrArgAlaIaVal 697
DB 2014 ATCAAGGCTGATTGSGGTAAACAATGTTTCGAGATCGAGCTTGCGCAACTGTGCTTATC 2073
QY 698 GluAsnThrSerGlyArgGlyPhePheGlnGlnTyrTyrProPheValIleValGlnAla 717
DB 2074 CAACAGATCTTCTCTC---CTATTGATATGATCTACCTTCTGTAAGTTTCACTT 2130
QY 718 ValTyrAlaArgGlnAspSerPheValGlnLeuGlyAla---IleSerArgAspPheSer 736
DB 2131 GTCGATACGACCAACATGATGACTTAAAGAAACAAATAGCATCAGGAAAGATATCTCGAA 2190
QY 737 AspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLeuLeuGlnIleAspArgPheAla 756
DB 2191 AGCAGAAATCTACCAACTTCTCTGCTATCGGATCGGATCAAGTTTGA---AGATTGTCT 2247
QY 757 GluGln-----TyrTyrHisValAlaIleMetTyrSerProAspValCysArgSer 773
DB 2248 AACACGATACAGCTTCTTATCATGCTCACTGCTTATCTCTGATATCTGTAAGAGT 2307
QY 774 AsnProLysCysThrThrThrLeuLeuSerAsnGlnGlySer-----TyrLysThrLys 791
DB 2308 AACCTGACTGACTACTCTCTGTTAGTAAAGCCCGACCTGCTGCTGCGGTAAAGAAA 2367
QY 792 GlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGly 811
DB 2368 GCCAACACCTTCGCGAGCGCTTCATGCTACAGACGAAACTACTGTTTAACT 2427
QY 812 AlaAlaAlaGlnLeuPheGlyAsnPheGlyPheGlnTyrPalaGlySerSerArgSerTyr 831
DB 2428 CACAACATAGAAATCTTCAGCCAGCTTCGTTTCAGACTCAGGGGATCTTCAAGAACTAT 2487
QY 832 AsnValAspAlaGlySerIleLysPhe 841
DB 2488 AACGTAGATCTCGATCGAAGATCCAGTTC 2517

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RESULT 6
US-10-312-273-116

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/ Sequence 116, Application US/10312273
/ Publication No. US20040005667A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
/ FILE REFERENCE: P025035W0
/ CURRENT APPLICATION NUMBER: US/10/312,273
/ PRIOR FILING DATE: 2002-12-20
/ PRIOR APPLICATION NUMBER: 0016363.4
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 0017047.2
/ PRIOR FILING DATE: 2000-07-11
/ PRIOR APPLICATION NUMBER: 0017983.8
/ PRIOR FILING DATE: 2000-07-21

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/ PRIOR APPLICATION NUMBER: 0019368.0
/ PRIOR FILING DATE: 2000-08-07
/ PRIOR APPLICATION NUMBER: 0020440.4
/ PRIOR FILING DATE: 2000-08-18
/ PRIOR APPLICATION NUMBER: 0022583.9
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: 0027549.5
/ PRIOR FILING DATE: 2000-11-10
/ PRIOR APPLICATION NUMBER: 0031706.5
/ PRIOR FILING DATE: 2000-12-22
/ NUMBER OF SEQ ID NOS: 664
/ SOFTWARE: SeqWin99, version 1.02
/ SEQ ID NO 116
/ LENGTH: 2787
/ TYPE: DNA
/ ORGANISM: Chlamydia pneumoniae
/ US-10-312-273-116

Alignment Scores:
Pred. No.: 7,71e-137 Length: 2787
Score: 1435.50 Matches: 340
Percent Similarity: 51.43% Conservative: 147
Best Local Similarity: 35.90% Mismatches: 335
Query Match: 33.42% Indels: 125
DB: 12 Gaps: 15

US-09-830-446-27 (1-841) x US-10-312-273-116 (1-2787)
QY 1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
DB 1 ATGAAGACTTCGATTCCTTGSGTTTATGTTCTCCGCTTACGCTTCTCA---TGTCAC 57
QY 21 LeuLeuGlyAlaAlaThrThrGlnGlnLeuSerAlaSerAsnSerPheAspGlyThrThr 40
DB 58 CTACAGTACACTAGCTAACAGAGAACTTTATCACTGATATAGTTTAATGAAATATC 117
QY 41 SerThrThrSerPheSerSerLysThrThrSerSerAlaThrAspGlyThrAsnTyrAlaPhe 60
DB 118 GATTCAGGAGACGTTTACTCCAAAACCTTCAGCC-----ACAACTATATCTCTA 165
QY 61 LysAspSerValIleGlnAsnValProLysThrGlyGlnThrGlnSerThrSerCys 80
DB 166 ACAGAGATGTCCTTCTTTTACAG---CTGAAAAGCACTCCTTATGACAGTTGT 222
QY 81 PheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyPheSerPheThr 100
DB 223 TTTAAGCAA-----ACACGAGCAATCTTACCTTCTGGGAAAGGTCATAGCTTAAG 276
QY 101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGlnAlaAsn 120
DB 277 TTTGGCTTTATAGATGCTGCGACATCATCAGGTGCTGCT---GCATCTTAACAAGCAAT 333
QY 121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
DB 334 AAGAACTTACCTTCTCAGGGGTTTCTTACTGAGTTTGAATTCCTCTTCAGCAACAG 393
QY 141 ValThrAsnGlyLeuGlyAlaIleAsnValIysGlyAsnLeuSerLeuLeuAspAsnAsp 160
DB 394 GTTACTACAGGTCAAGGAAAGCGTTTCTCAGCAGAGAGCGTAATTTGAAATATTTGT 453
QY 161 LysValLeuIleGlnAspAsnPheSerThrGlyAspGlyAlaAlaIleAsnCysAlaGly 180
DB 454 AAACCTGTAGTTGCTGGAATTTTCTTACTCAGATGCTGAGGCTATCAAGAGACGCT 513
QY 180 ----- 180
DB 514 TTCCTTTAAGTGGACTTTCGAGAGTCTTTTATGTAACAACCTTCAACAAG 573
QY 180 ----- 180
DB 574 GAGAGCAATTTGCTACTACAGCAGCGCTGCAATAGCAATTAACAAGTTATGTAGA 633
QY 180 ----- 180

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Db 634 TTCCTATCTAACTACGCTCTACGAGAGGCGCTATGATGATGAGGACGTCGATA 693
 Qy 180 ----- 180
 Db 694 CTATCGAACACAAATTTCTATATTTTGAAGGAAATGACAGCGAAAATCTAGCGCGTGG 753
 Qy 181 -----SerLeuLysIleAlaAsnAsnLysSerLeu 190
 Db 754 ATCTGCACACCAAGGAGGAGTGTCTCTGAACTGATATATCTCTAACTAATGAAGCTCTG 813
 Qy 191 SerPheIleGlyAsnSerSerSerThrArgGlyValAlaIleHisThrLysAsnLeuThr 210
 Db 814 ATCTTGCTTCAACCTACAGAAACAGACGGTGGCGCATCCATCCTAAAGCTAAAGCC 873
 Qy 211 LeuSerSerGlyGlyValThrLeuPheGlnGlyAsnThrAlaProThrAlaIleGlyLys 230
 Db 874 CTTTCTCTCGAGGCTTTACAGAGTTTCAAGAAATATGTCATCAGCACTCCTTAAG 933
 Qy 231 GlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSerGlyAsp 250
 Db 934 GGGGGGCTATACGATCGATCGCTCAGAGAGCTCAGTCTTCTGACAGACAGAGAAAC 993
 Qy 251 IleIlePheGlnGlyValSerThrIle-----GlyAlaThrGlyThrValSerHisSer 267
 Db 994 ATTACCTTGTAAAGAAATACCTTACACAAACCGAAGTACCGATCTCTAAACGTAAT 1053
 Qy 268 AlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaIleGlnGlyHisThr 287
 Db 1054 GCGATCAACATAGAGAGTAAACGGAAATTCACCGAATTACGGGCTCTAAATCTAACA 1113
 Qy 288 IleThrPheThrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsn 307
 Db 1114 ATTTCTCTCATGATCCCATCTCATCTCAGAAAGAACTCATCA-----GACGTAATGAAG 1167
 Qy 308 IleAsnSerProAspThrGlyAspAsnLysGlyValThrGlyThrIleValPheSerGly 327
 Db 1168 ATAAATAAACGGCTCTGCGGAGCTCTCAATCCATATCAAGAAACGATTTCTATTTCTGA 1227
 Qy 328 GlyLysLeuThrGlyAlaGlyAlaLysAspGlyLysAsnArgThrSerLysLeuLeuGln 347
 Db 1228 GAACCTTAACACAGATGAACTTAAGTTCGACAACTTAATATCTTCATTCACCGAG 1287
 Qy 348 AsnValAlaPheLysAsnGlyThrValAlaLeuLysGlyAspValAlaLeuSerAlaAsn 367
 Db 1288 CCAAGTCCCTATCCGAGGAGAAAGTATATGCTACAAAGGAGACTCATTTAAGAGACAG 1347
 Qy 368 GlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeuValAla 387
 Db 1348 AGCTTCTTCAAGAGCGCGTCTCTCTCGCATGATTCAGAGAACGACATTATCAACT 1407
 Qy 388 AsnThrGlnSerIleGlyLeuThrAsnLeuGlyAlaAsnIleAspSerLeuArgAsnGly 407
 Db 1408 ACACGCTGGAGATTTCAATCACGAACCTTAGGAATCAAGTACCTTAAAGCTTTAAG 1467
 Qy 408 LysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAspArgProVal 427
 Db 1468 CAGCCGCTCAGCTTACACAGAAAGGTCTCAAAATTAAGTATGCTAAGCTGGAGAGCTC 1527
 Qy 428 ValLeuAlaIleSerAspGlySerPheTyrgLysAsnGlyPheLeuAsnGlyLysAspHisSer 447
 Db 1528 AACCTATGATTAATGAGGAAACATTTATGAAGATCATATGTTTCAGCATGACGAGCTC 1587
 Qy 448 TyrAspGlyIleLeuGlyLeuAspAlaGlyLysAspIleValIleSerAlaAspSerArg 467
 Db 1588 TTC---TCTCTATTAATAATCAACGTTGATGCTGAGTGAATCTAAGCTGATCAGC 1644
 Qy 468 SerIleAspAlaVal-----GlnSerProTyrgLysGlnGlyLysTyr 482
 Db 1645 AGCTTATCCCGTTCCTGCTGAGATCCAAATTCAGAAATAGAGATTCGAAGACAAATGG 1704
 Qy 483 ThrIleAsnTyrSerThrAsp-----AspLysLysAlaThrValSerTyrAla 498

Db 1705 AATGTTAATGGACTACGATACAGCTACAAATACAAAAGAGCCACGGCAACTTGGACC 1764
 Qy 499 LysGlnSerPheAsnProThrAlaGlnGlnGlyAlaProLeuValProAsnLeuLeuTyr 518
 Db 1765 AAAACAGATTTGTTCCGAGCCCCGAAAGAAATCTGCGTTAGTATGCAATACCTATGG 1824
 Qy 519 GlySerPheIleAspValArgSerPheGlnAsnPheIleGlnLeuGlyThrGlnGlyAla 538
 Db 1825 GGAAGCTTACTGACATTCGCTCTGCAACAGCTTGTAGATGCGGCCAACCTGGTATG 1884
 Qy 539 ProTyrgLysArgPheThrValAlaGlyIleSerAsnValLeuHisArgSerGlyArg 558
 Db 1885 GAACACAAACAAAGTTTCTGGGTTTCTCCATGACAGAACTTCTGCTAAGACTGGAGAT 1944
 Qy 559 GlnAsnGlnArgLysPheArgHisValSerGlyGlyAlaValAlaGlyLysSerThrArg 578
 Db 1945 GAAATATCGAAAGGCTCCGCTCATACCTGAGAGCTACGTATCATCGGTGAGTGTCTAC 2004
 Qy 579 MetProGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAsp 598
 Db 2005 ACTCTAAAGACGACTATTTCACCTTGGGTTCTGCCATCTCTTGTGTAAGACAAAGAT 2064
 Qy 599 TyrPheMetAsnThrAsnPheAlaLysThrTyrgLysSerLeuArgLeuGlnHisAsp 618
 Db 2065 TGTATTATGCTCACAACTCTGAACTTACGGTGAACCTTATCTTCAAGACTCT 2124
 Qy 619 AlaSerLeuTyrgSerValSerIleLeuLeuGlnGlyGlyLysLeuArgGlyLysLeu 638
 Db 2125 CATACCTTAACAAACCCAAACATTTAGATTAGGAAGACAAAGTTTCTGAATCAGCT 2184
 Qy 639 LeuProTyrgValSerLysThrLeuProCysSerPheTyrgLysGlnLeuSerTyrgLys 658
 Db 2185 ATAGAAATATCCCTAGGAAATTCCTCCTAGCTTGGATGTCAAAGTTTGTTCAGACCAT 2244
 Qy 659 ThrAspHisArgMetLysThrGlu-----SerLeuProProProProThrLeuSer 676
 Db 2245 TCAACACACCGTATGAAACGCACTATACCTCATTTGCCA----- 2283
 Qy 677 ThrAspHisSerThrProGlyTyrgValAlaThrAlaGlnGlyLeuGlyThrArgValAla 696
 Db 2284 GAATCGGAAGTCTTGGAGCAACGAGTGTATAGTGGTATGAGGCTTACCTCTCT 2343
 Qy 697 ValGlnAsnThrSerGlyArgGlyPhePheGlnGlyTyrgThrProPheValLysValGln 716
 Db 2344 TTGTGTTCTTCAACCCACATCTCTTTCAGAGCTTTCATTCACAGATGAAGCGAA 2403
 Qy 717 AlaValTyrgAlaArgGlnAspSerPheValGlnLeuGlyAlaIleSerArgAspPheSer 736
 Db 2404 ATGGTTATGATCACAAAATAGCTTCTGAAAGCTCTAGATGAGCCGTGTTTACT 2463
 Qy 737 AspSerHisLeuTyrgAsnLeuAlaIleProLeuGlyLysLys-----LeuGlnLysArgPhe 755
 Db 2464 ATTGGAAGCTCTTAACCTTCGATTCCTGTGGTGGCAAAATTCGTGAGGGGAGATAC 2523
 Qy 756 AlaGlnGlnTyr---TyrgHisValAlaMetTyrgSerProAspValCysArgSerAsn 774
 Db 2524 GGAAGATTCCTACACTATGATCTCTCAGGATCTTGTGTTCCGAGTGTATGTAACAT 2583
 Qy 775 ProLysCysThrThrThrLeuLeuSerAsnGlnGlySerTyrgLysThrLysGlySerAsn 794
 Db 2584 CCCCAATCTACAGCAGACTCTTGATGAGCCAGACTCTTGAAATTAATTCGCGGTGGCAAT 2643
 Qy 795 LeuAlaArgGlnAlaGlyIleValAlaGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAla 814
 Db 2644 CTTTCAAGACAGCACTTTTACTGAGGGGTACCAACAATAGCTACAACTCCAACTTGT 2703
 Qy 815 GlnLeuPheGlyAsnPheGlyPheGlyLysTyrgLysSerTyrgSerTyrgAsnValAsp 834
 Db 2704 GAGCTTCTGCAATTCATTCAGAACTCCGTGATCTTCAAGAACTACATGATGAT 2763
 Qy 835 AlaGlySerLysIleLysPhe 841
 Db 2764 GTTGTACCAAACTCGAATTC 2784

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RESULT 7
US-10-312-273-46
; Sequence 46, Application US/10312273
; Publication No. US200400567A1
; GENERAL INFORMATION:
; APPLICATION: CHIRON SPA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035W0
; CURRENT APPLICATION NUMBER: US/10/312.273
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 46
; LENGTH: 2793
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-46

Alignment Scores:
Pred. No.:      8,79e-135      Length:      2793
Score:          1415.50       Matches:      352
Percent Similarity: 50.53%    Conservative: 129
Best Local Similarity: 36.97%  Mismatches:   338
Query Match:     32.96%      Indels:       133
DB:              12          Gaps:           19
US-09-830-446-27 (1-841) x US-10-312-273-46 (1-2793)

Cy 1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
Db 1 ATGAAATAACCTTGACAAACTCTGATCTCT-----TCGACTCTGTGCACTCCCAAT 54
Cy 21 LeuLeuGlyAlaIleThr-----ThrgIuGluLeuSerAlaSerAsnSerPheAsp 37
Db 55 CTATTAGACATTGCAACTTACGAGACAGATGCTTTATTCCTCCACGATAGCTTTAT 114
Cy 38 GlyThrThrSerThrThrSerPheSerSerlyThrSerSerAlaThrAspGlyThrAsn 57
Db 115 GGAGCGCGCGCTCTACA---TTTACTCCAAATCTACAGCAGATGCCAATGAAACGAAAC 171
Cy 58 TyrValPheIleAspSerValIleIleGluLeuValProIleThrGlyIleThrGlnSer 77
Db 172 TATGCTTATACAGAAATGCTATATTAACGATGCTGGAAA---GGCAGCATTAACA 228
Cy 78 ThrSerCysPheIleAsnAspAlaIleAlaIleAspLeuAsnAsnPheLeuGlyGlyPhe 97
Db 229 GCGTCTCTCTTACGAA-----ACTACGGGTATCTGACCTTACGGAAGGAGATAC 282
Cy 98 SerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaIleIleGlySerGlu 117
Db 283 TCATTTCATTCACACACGATAGATCGGGGTTCGAATGACAGAGCTGCG---GCAAGCACA 339
Cy 118 AlaIleAsnIleThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuIleSerPro 137
Db 340 ACTGCTGATTAAGCCCTTAACATTCACAGGATTTTCAACCTTCCATCATGACAGCTCT 399

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Cy 138 AlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValIleAsnIleAsnLeuSerLeu 157
Db 400 GGAACACTACAGTTGGCTGAGGAAAAAGTACTTAAAGTCTCAGAGAGGCTTAATCTTACC 459
Cy 158 AspAsnAspIleValIleIleGlnAspAsnPheSer----- 169
Db 460 GATAATGAAACGATTCCTTTAGCCAAACGCTCCCAATGAACTAATAACAATGGCGGA 519
Cy 169 ----- 169
Db 520 GCGATCACCAAAAACTCTTCTATTTCTGGGAATACCTCTCTAATACCTTCACTAGT 579
Cy 169 ----- 169
Db 580 AATAGCGCAAAAAAATTAGGTGAGCGATCTATAGCTCGCGGTGCAAGTATTTACAGA 639
Cy 169 ----- 169
Db 640 AACACCGGCGAGTATGCTTTATGATATTAAGAGAAACCTGGGGGTGGGCTTGCGGC 699
Cy 169 ----- 169
Db 700 TTGAAAGCAGCTCTCGATTAACCAAAATAGCTCCCTTTCTCTCGGAAACACTGCA 759
Cy 170 -----ThrgIleAspGlyGlyAlaIleAsnCys-----AlaGlySer 181
Db 760 ACAGATCTGCAAGGCAAGCGCGGCGCATTTATGTGAAAAACAGAGAGACTCTACT 819
Cy 182 LeuIleValIleAsnAsnIleSerLeuSerPheIleGlyAsnSerSerThrThrArgIly 201
Db 820 CTTAATCTCTCTGAAATTAAGCTGACCTTGCCGAGAACTCTTACGTAATCAAGGCG 879
Cy 202 GlyValIleIleThrIleAsnLeuThrLeuSerSerGlyGlyGlyIleThrIlePheGly 221
Db 880 GAGCAATCTGTGCGCCATGCTGATCTTATCTTCCGCTGCGCCCTACCTATTTTCAAT 939
Cy 222 Asn---ThrAlaProThrAlaIleGlyIleGlyAlaIleAlaIleAspSerGly 240
Db 940 AATAGATCGCGGAACACAGCTGACGAGCAAGCGCGCTATTTGCAATTCGCACTTGA 999
Cy 241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAla 260
Db 1000 TCTTAAGTCTCTCTGCAAAATCAAGAGACATCAAGTCTTGCAACACTTCACTCA 1059
Cy 261 ThrGly-----ThrValSerHisSerAlaIleAspLeuGlyThrSerAlaIleThr 278
Db 1060 ACTTCGCGCGCAACATGACACGAAATGCTATCTTACCTGGATGTCAGCAAAATTAACG 1119
Cy 279 AlaLeuArgAlaIleGlnGlyIleThrIleTyrPheIleThrAspProIleThrValThrGly 298
Db 1120 AACTTAAGGAGCGCAAGCGCAATCTATCTATTTCTATGATCCGATTT---GCATCTAAC 1176
Cy 299 SerThrSerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnIleGlu 318
Db 1177 ACCACAGAGAGCTTCAAGCTTGTACCATCAACACCGATACCACTCGCTTTAGAT 1236
Cy 319 TyrThrGlyThrIleValIlePheSerGlyIleIleThrIleIleGluAlaIleAspGly 338
Db 1237 TATTCAGAACGATGTGATTTTCTGGGAAAAAGCTCTCTGACATGAGCAAGAGCTGCT 1296
Cy 339 LysAsnArgThrSerIleLeuLeuGlnAsnValAlaIlePheIleAsnGlyThrValIleLeu 358
Db 1297 GATTAACCTTACATTAATTAAGCAACATTTGCTCTAGCTCTGGAACCTTGACACT 1356
Cy 359 LysGlyAspValIleLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerIleLeuIle 378
Db 1357 AAAGAAATGTCGAGTGAATGTCAAATGTTTCAACAGACTGAAGGCTTACACTCTC 1416
Cy 379 MetAspLeuGlyThrSerLeuValAlaAsnThrGlyIleIleGluLeuThrAsnIleGlu 398
Db 1417 ATGCAACCGAAGCAAAAGCTTAAGCAAGATCTAAGCTATCACTTACCAAACTTCTC 1476
Cy 399 IleAsnIleAspSerLeuArgAsnGlyIleIleValIleIleIleSerAlaIleThrAlaGln 418

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Oy 60 PheIysAspSerValIleGluAsnValProIysThrGlyIuThrGlnSerThrSer 79
Db 175 CTGACAGGAAATATACCTGCAAAACCTT-----GGGAAATCGCGACCTTTAACG 225
Oy 80 -----CysPheIysAsnAspAlaIleAlaGlyAspLeuAsnPhelGlyIleGlyPhe 97
Db 226 AAGGGTGTGTTTCTGACACTACGGAATCT-----TTAAGCTTGGCGGTAAAGGGGTAC 279
Oy 98 SerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaIleGlySerGlu 117
Db 280 TCATCTCTTTTAAAAATATT-----AAGCTAGTGTGAAAGGCGACACTT---TCGTGT 333
Oy 118 AlaIleAsnIleThrValThrIleuSerGlyPheSerAlaIleuSerPheIleuSerPro 137
Db 334 ACAACTGATTAATAATCTCTCGCTAACAGATTTCGACTTACTTCTTACCGGCCCA 393
Oy 138 AlaSerThrValThr-----
Db 394 TCATCGGTAATCACAAACCCCTCAGAAAAGGTGCAATTAAATGAGGAGGATCTTACA 453
Oy 143 -----AsnGlyLeu-----
Db 454 TTTGATTAACAATGAACTATTATTATAACAAGATTACTGTGAGAAAATGCGGAGCC 513
Oy 145 -----
Db 514 ATTCTCAACAAGAACTCTTCTTGAAAACAGCAAGGATGCAATTCTTTGAAAGGAAT 573
Oy 145 -----
Db 574 AAATCGACGCAACAGGAAAAAGTGGGCTATTGCTACTGTAAGTATGATATT 633
Oy 146 -----GlyAla 147
Db 634 ACAAAATAATACGGCTCTACCTCTTCTGAACAATATTCTGAAGCTGACGAGTGAGCT 693
Oy 148 IleAsnValIysGlyAsnLeuSerLeuAsnAspIleValIleuIleGluAsnAsn 167
Db 694 ATTAATACACAGGAACTGTACATTTACAGGAAATAGCTCTCTTGTATTTTTCGAAAT 753
Oy 168 PheSerThr-----GlyAspGlyIleAlaIleAsnCysAlaGlySerLeuIle 184
Db 754 AGTGTGACAGCGACCGCAGAAATGAGAGAGCTCTTCTGAGATGCGGATGTTACATA 813
Oy 185 AlaAsnAsnIysSerLeuSerPheIleGlyAsnSerSerThrArgIleGlyAlaIle 204
Db 814 TCTGGAAATCAGAGGTAACTTCTCAGGAAACCAAGCTGACTAATGCGGAGCCATT 873
Oy 205 HisThrIysAsnLeuThrIleuSerSerGlyIleuThrIleuPheGlnIleGlyAsnThrAla 224
Db 874 TATGCTAAGAACTTACACTGCTCCGGGGG-----GGGGGGGTATCT 918
Oy 225 Pro-----ThrAlaIleGlyIleGlyAlaIleAlaIle 236
Db 919 CTTTTTCTTAACAATATAGTCCAGAGTACCACTGCAAGGTAAAGTGGAGCCATTCTATA 978
Oy 237 AlaAspSerGlyThrIleuSerIleSerGlyAspSerGlyAspIleIlePheGlnIleuAsn 256
Db 979 CTGGACGCTGAGAGGTATGCTTCTCAGCAAGAACGAGGACATTACCTTCAATGGGAAT 1038
Oy 257 ThrIleGlyAlaThr-----GlyThrValSerHisSerAlaIleAspLeuIleThrSer 274
Db 1039 GCCATTGTTGCAACTACCAACAACCACTCAAAAAGAAATTCATTATGACATAGGACTACT 1098
Oy 275 AlaIleValIleThrAlaIleuAlaIleGlnIleGlyIleThrIleThrPheIleAspProIle 294
Db 1099 GCAAAAGATCACAATTAATGATCTGCGGACATGATCTTTTCTTACCATCCGAAAT 1158
Oy 295 ThrValThrGlySerThrSerValAlaAspAlaIleuAsnIleAsnSerProAspThrGly 314
Db 1159 ACTGCTAATACGGCTGCGGATTTCTACAGTACTTTAAATCTCAATTAAGGCTATGCAAGT 1218

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Oy 315 AspAsnIysGlyThrGlyThrIleValPheSerGlyIleuIleuThrGluAlaGlu 334
Db 1219 AATAGTACAGATTAATATAGTGGCTGATTTGTTTCTGTGAAAAAGCTCTCGAAGATGAA 1278
Oy 335 AlaIysAspGlyIysAsnArgThrSerIleuIleuGlnAsnValAlaPheIysAsnGly 354
Db 1279 GCAAAAGTTGCAACAACCTCCTTACCTTACAGAGGCTGTACTTACCTTACAGAGGA 1338
Oy 355 ThrValIleuIysGlyAspValIleuSerAlaAsnGlyPheSerGlnAspAlaAsn 374
Db 1339 AATTATGACTTAACACTGGTGTACCTCGATACGAAAGGCTTACTACAGCGGGGT 1398
Oy 375 SerIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 394
Db 1399 TCTCTGTATTAATGATGCGGCGACAACTTAAGCAAGTACAGAGGATCACTTTA 1458
Oy 395 ThrAsnLeuGluIleuAsnIleAspSerLeuAsnGlyIysValIleuIleuSerAla 414
Db 1459 ACAGTCTTTCATTCCTGTAGACTTTTAGCGCAGAGGTAAAGAAAGTTGTAATGCTGT 1518
Oy 415 AlaThrAlaGlnIysAspIleArgIleAspArgProValIleuAlaIleSerAspGlu 434
Db 1519 TCTGACCAAGTAAATAATGATAGCCCTTAGTGTCCGATCTTCTTTGATTAACCAAGG 1578
Oy 435 SerPheIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 454
Db 1579 AATGCTTGAATAATCAGCACTTAGAATAAATCAAGACTT---TCATTGTGCACTTC 1635
Oy 455 AspAlaGlyIysAspIleValIleSerAlaAspSerArgSerIleAspAlaValGlnSer 474
Db 1636 TCTGCT---CTGGTACTGCAACAACCTACAGATGTTCCAGGGTCTTACAGTAGCACT 1692
Oy 475 Pro-----TyrGlyIleGlnIleuIleuIleuIleuIleuIleuIleuIleuIleu 489
Db 1693 CTTACGCACTATGAGTATCAAGTACTTGGGAAATGACTTGGTGTATGATACCGCAAGC 1752
Oy 490 -----AspIysValIleThrValSerThrAlaIysGlnSerPheAsnProThrAla 506
Db 1753 ACTCCAAGACTAAGACAGCGACACTTAGCTTGACATACAGCTCTTCCCAATCT 1812
Oy 507 GluGlnIleuAlaProIleuValProAsnLeuIleuIleuIleuIleuIleuIleuIleu 526
Db 1813 GAGGCTAAGACCTTTAGTCTTAATAGCTTGGGATCTTTTTCAGACATCAAGCG 1872
Oy 527 PheGlnAsnPheIleGluIleuGlyThrGluGlyAlaProIleuIleuIleuIleuIleu 546
Db 1873 ATTCAAGGTGCATAGAGAGAGAGCTTTGACTTTTGTTCAGATCAGAGCTTGGGCT 1932
Oy 547 AlaGlyIleSerAsnValIleuHisArgSerGlyArgGluAsnGlnArgIysPheArgHis 566
Db 1933 GCGGAGAGCGCCAAATTTCTTATGATTAAGATTAAGAAAGGCGAAACCCCAATACCGTCA 1992
Oy 567 ValSerGlyIleAlaValIleGlyAlaSerThrArgPheProGlyIleAspThrIleuSer 586
Db 1993 AAATCTGTGTATATGCTATGAGAGGTGACGCGCAAACTTGTGAAACTTAAATTAGC 2052
Oy 587 LeuGlyPheAlaGlnIleuPheAlaArgAspIysAspIlePheMetAsnThrAsnPheAla 606
Db 2053 TTTGCCCTTTGCCAACTCTTGTGATGAGATTAAGATTTCTTAGTCGCGTAAAAATCATACT 2112
Oy 607 LysThrIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 626
Db 2113 GATACCTATGACAGAGCTTCTATATACCAACACTTACAGATGATAGTGGGTATAGT 2172
Oy 627 IleLeuIleuGlyIleuGlyIleuArgIleuIleuIleuIleuIleuIleuIleuIleu 646
Db 2173 TGTCTCTTAATTA-----CTTCTGCTCTTGGAGTATATA 2211
Oy 647 ProCysSerPheIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 666
Db 2212 CCCCTCGTTTGAAGAGGCACTGCTTATAGCAACGTCATTAATGATGTAAAGCAAG 2271
Oy 667 SerLeuProProProProProThrIleuSerThrAspHisThrSerIleuIleuIleuIleu 686

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Db      2272 TATAGTCCATCTGAGGCG-----AAAGTCTCTGGGGAATATAGCT 2316
Qy      687 TTPALAGLGLuLGLYThrArgValAlaValGluAenThSerGlyArgGlyPhe--- 705
Db      2317 TTTAACATGATGTGGG-----GCTTCTTCTCATTTATCTCT 2355
Qy      706 -----PheGlnGluYrThrProPheValIleValGlnAlaValIleValAla 720
Db      2356 GAATACCTGCACTTTTATGATCTATGCTCCATCATCATCAATCAATGACCTATATA 2415
Qy      721 ArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSerAspSerHisLeu 740
Db      2416 CCGACAGACAGCTTCTCGAGAAAGGATACAGAAAGAAAGATCTTTGATGACAGCAACCTC 2475
Qy      741 TyrAsnLeuAlaIleProLeuGlyIleIleGluGluIleArgPheAla-----Glu 757
Db      2476 TTCATTTATCTTGTGCTTATAGGGGTGAAGTTTGAGAG---TTCCTGATGTATATGAC 2532
Qy      758 GlnYrYrThIleValAlaValAlaMetTyrSerProAspValCysArgSerAsnProIleCys 777
Db      2533 TTTTCTTATGATGATCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCTTATGCT 2592
Qy      778 ThrThrThrLeuLeuSerAsnGlnGlySerTyrPheSerThrIleGlySerAsnLeuAlaArg 797
Db      2593 ACTACAGCACTTGTATATACAGCGAGCGCTCTTGGGAAACTATGCCAATATCTTAGACCA 2652
Qy      798 GlnAlaGlyIleValAlaIleAsnSerGlyPheArgSerLeuGlyAlaAlaIleGluLeuPhe 817
Db      2653 CAGGCTTCAAGTGTGGTACAGCACTCACTACGCTTCTCTCTATGTTTGAAAGTCTC 2712
Qy      818 GlyAsnPheGlyPheGluTyrPargIleSerSerArgSerTyrAsnValAspAlaGlySer 837
Db      2713 GGCAGCTTGTCTTATAGCTTGTGATCTCTGATCTTATCCGCAATGATCCCAATGCT 2772
Qy      838 LysIleLysPhe 841
Db      2773 AAGTTCCAATTC 2784

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Db

Qy

US-10-312-273-34

Sequence 34, Application US/10312273

Publication No. US20040005667A1

GENERAL INFORMATION:

APPLICANT: CHIRON SPA

TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE

FILE REFERENCE: P025035WO

CURRENT APPLICATION NUMBER: US/10/312,273

PRIOR FILING DATE: 2002-12-20

PRIOR APPLICATION NUMBER: 0016363.4

PRIOR FILING DATE: 2000-07-03

PRIOR APPLICATION NUMBER: 0017047.2

PRIOR FILING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: 0017983.8

PRIOR FILING DATE: 2000-07-21

PRIOR APPLICATION NUMBER: 0019368.0

PRIOR FILING DATE: 2000-08-07

PRIOR APPLICATION NUMBER: 0020440.4

PRIOR FILING DATE: 2000-08-18

PRIOR APPLICATION NUMBER: 0022583.9

PRIOR FILING DATE: 2000-09-14

PRIOR APPLICATION NUMBER: 0027549.5

PRIOR FILING DATE: 2000-11-10

PRIOR APPLICATION NUMBER: 0031706.5

PRIOR FILING DATE: 2000-12-22

NUMBER OF SEQ ID NOS: 664

SOFTWARE: SeqWin99, version 1.02

SEQ ID NO 34

LENGTH: 2787

TYPE: DNA

ORGANISM: Chlamydia pneumoniae

US-10-312-273-34

Alignment Scores:

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Pred. No.: 4,396-131 Length: 2787
Score: 1379.50 Matches: 348
Percent Similarity: 49.53% Conservative: 124
Best Local Similarity: 36.52% Mismatches: 344
Query Match: 32.12% Indels: 137
DB: 12 Gaps: 22

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US-09-830-446-27 (1-841) x US-10-312-273-34 (1-2787)

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Qy      1 MetLysIleProLeuArgPheLeuLeuIle-----SerLeuValProThrLeuSerMet 18
Db      1 ATGAATCTCTCTCTCATGTTTAACTCGTCATCTTTAGCACTTCCCTGACACTA 60
Qy      19 SerAsnLeuLeuGlyAlaIleThrArgIle---GluLeuSerAlaSerAsnSerPheAsp 37
Db      61 AATTCTCGCGTTTGGCTGCTGCTGTTGTAATCAATCTAGAGCACTTACCAATAGCTTCT 120
Qy      38 GlyThrThrSerThrThrSerPheSerSerIleThrSerSerAlaThrAspGlyThrAsn 57
Db      121 GGACCAAGAACTACACTCTCCACGCCCAACAAACAAATGCA-----GATGAACTATC 174
Qy      58 TyrValPheLysAspSerValIleGluAsnValProLysThrGlyIleThrGlnSer 77
Db      175 TATATCTTAAACAGGAGATGCTCAATCAACCAATGCA---GATCTCCGACAGCTTAACC 231
Qy      78 ThrSerCysPheLysAsnAspAlaAlaIleGlyAspLeuAsnPheLeuGlyIleGlyPhe 97
Db      232 GCTTCCTGCTTAAAGAA-----ACTACTGGAAATCTTCTTCCAGAGCCACGCTAC 285
Qy      98 SerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGlu 117
Db      286 CAATTCCTCTCAAAATATGATGATCG-----GGAGCAACTGTACCTTACCAATACA 339
Qy      118 AlaIleAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerPro 137
Db      340 GCTGCAAAATTAACCTCTCTCTTTCAGGATCTCTCTTATTTGCTCACTAATCAAAAC 396
Qy      138 AlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeu 157
Db      397 ---ACGAATGCTACACAGAAACAGAGCATCAAGTCCACAGAGCTTGTCTATTCAG 453
Qy      158 AspAsnAspLysValLeuIleGlnAspAsnPheSer----- 169
Db      454 TCGAATCTATAGTGTCTACTTGGCCAAACTTTTCTAATGACATGAGAGCCCTCCAA 513
Qy      169 ----- 169
Db      514 GGCAGCTATCAGTCTATCGCTAAACCCCACTACGTTGCCAAAAACAAGACAG 573
Qy      169 ----- 169
Db      574 CAAAAAGGGGGTCCCTCTATTCCAGGGAGGATTAACAATTACATTACGTTAAACTCA 633
Qy      169 ----- 169
Db      634 GCATCATTTTCTGAATAATACCGCGGCAACATGCGGAGCATTTTACAGSAGACTAGC 693
Qy      170 -----Thr 170
Db      694 AGTTTATTAGACAGCAACAAGCAATTAGCTTATTAACAATAGTGTACCGCAACTCA 753
Qy      171 GlyAspGlyGlyAlaIleAsnGlyAlaGlySer-----LeuLysIle 184
Db      754 GCTACAGGGGGAGCCATTACTGTAGTATGATCATAGCCGCCCAACACAGCTTAACTCA 813
Qy      185 AlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArgGlyIleAlaIle 204
Db      814 TCGACACAGCGGAACTGACTTATAGGAATACAGCAATTAAGTCTAGTGTGGCGGAT 873
Qy      205 HisThrLysAsnLeuThrLeuSerSerGlyIleGluThrLeuPheGlnGlyAsnThrAla 224
Db      874 TATAGTCAACATCTAGTCTTCTTCTGAGAGACCTACGCTTTTAAAAACAACCTGCT 933

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Oy 225 ---ProthralaialglyylglylalaialaialaaspserglyThreuser 243
Db 934 ATAGATACGACGCTCCCTTAGAGAGAGCAATTCGATTCGACTCGACTTGAAGT 993
Oy 244 lleserglyaspserglyaspilalephegluglyasnthrile-----glyalathr 261
Db 994 CTTTCGGCTCTTGGTGAGACATCACTTTGAAAGAAACACAGTAGTCMAAGCACTTCT 1053
Oy 262 Gly-----Thrsalserhiseralailaspseugly---ThrsalalyalThr 278
Db 1054 TCGAGTCAGACCACTACGAAATTCATTAACATCGAAGAACCAACATGCTAAGATTGTA 1113
Oy 279 Alaleuargalalaglnglyaherhiletyrphetyrapproilethervalthrly 298
Db 1114 CAGCTGCAGGCTCTCAAGGCAATCTACTTCTAATGATCTTAACAACATGACATC 1173
Oy 299 SerthrservalAlaspAlaleuanilleasnserserproaspthrlyaspasnllysglu 318
Db 1174 ACTGACGCTCTCTAGATGCTCTAAACTAAATGATGCTGACCTTGACAGGAAATCTGCA 1233
Oy 319 TyrthrglythrileValPheSerglyylglyleuThrGluAlagluAlayaspGlu 338
Db 1234 TATCAAGAACCATGATTTCTGAGAGAAAGCTCTCGAAGCAAGAGCTGCAAGACT 1293
Oy 339 LysaenatgthrSerlyleuGluInasValAlapheylasnglyThrsValleu 358
Db 1294 GATATCTCAATCTACATTCAGCAACCTTAACCTTCGCGGAGGCACTCTCTT 1353
Oy 359 LysglyaspvalValleuserAlasnglyPheSerGluInasPalaasnseryleuile 378
Db 1354 AATCAGAGCTCTCTAGATGCTCTTAAGTCTTTTGCAATCTCCGGGCTTACCTCTCC 1413
Oy 379 MetaspseuglyThrseryleuValAlasanthrgluserileGluLeuThrAsnleuGlu 398
Db 1414 ATGATTCAGGAGCAACATTA---GAACCGCTGATGGAGATCAATCAATATCTTGT 1470
Oy 399 llaenillaspSerlyeuarasnglylylyllyleyleuserAlalathralagln 418
Db 1471 CTCATGTAGATTCCTTAAAGAGACCAAGAGGCTAAGCTTAAAGCAACACAGCAAGT 1530
Oy 419 LysaspilalehrgileaspargProValValleualilaseraspGluSerPheTyroln 438
Db 1531 CAGACAGCTCTTATCTGATGCTCTCTCTTGTAGATCTCTTGGAATATCTACGAA 1590
Oy 439 AsnglyPheleuAsngluAsphlaserTyraaspGlylileuGluLeuAspAlaglylys 458
Db 1591 GATGCTCTTGGAATTAACCTCAAGTCTT---TCTGTCTCATCTTACTGTCAGACAC 1647
Oy 459 AspilalealilaserAlaspserarSerileaspAlaValGlnSer-----Pro 475
Db 1648 CCGGGAATATTACATCAACATCACTAGCTGCTGATCCCTGAGAAAAAATCTATCAT 1707
Oy 476 TyrGlyTyrolnGlylylyserThrileasntp-----SerthraspAplys 491
Db 1708 TGGGATACCAAGGGAATTCGGCATATCTTGCAAGAGATATCGCATTAATCCAAA 1767
Oy 492 LysalathrValSerThrAlalyeglInserPheasnthrAlagluGlnGluAlaPro 511
Db 1768 GCAAGGACTCTTACTGCAAAACAGAGATCAATCCGAATCTGAGCTGTGAAACC 1827
Oy 512 LeuValProAsnleuLeuTyrGlySerPheileaspValarSerPheGlnAsnPhelile 531
Db 1828 TTAGTGTCAACACAGCTATGGGATCTTTGTGATGTCGCTCAATCAACAGCTTGTG 1887
Oy 532 GluleuGlyThrGluGlyAlaProTyrglylyasphetPvalAlaglylleseran 551
Db 1888 GCCACTAAAGTACGCCAATCTGAGAAACTCGGCGATCTGCTGGAAGGGATCTCGAAC 1947
Oy 552 ValLeuHlsarSerGlyTyrglyInasnglnarglylyPheargHlsValSerGlyAla 571
Db 1948 TTCTTCATTAAGATGACAGAGATTAATTAAGTTTCGACATTAAGTCCAGGTTAT 2007

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Oy 572 ValValGlyAlaSerThrArgMetProGlylyAspThrLeuSerLeuGlyPheAlaGln 591
Db 2008 GTTGAGAGGAGCATCAACAATCTTGATATCTTATCTTACAGGCTTGCCAA 2067
Oy 592 LeuPheAlaArgAspLyAspTyrrPheMetAsnthrAsnPhelAlalyThrTyrlagly 611
Db 2068 TTAATTCGGAAGATAGATGATCACTTAATAATAATAGAGCTTCGCTATGAGACT 2127
Oy 612 SerLeuArgLeuGlnHlsAspAlaserlyuSerValAlaserileLeuLeuGlyGlu 631
Db 2128 TCTCTCATCTCCAGCATCTAGCACTTG---TCTTCTCCAGCTTGACG----- 2178
Oy 632 GlyGlyLeuArgGluileLeuLeuProTyrrValSerlyThrLeuProCysSerPheTyrr 651
Db 2179 -----TACCTTCCTGATCTGAAGTGAAGAGCCGCTGCTTGTAT 2220
Oy 652 GlyGlnLeuSerTyrglyHlsThrAspHlsArgMetlyThrGluSerLeuProProPro 671
Db 2221 GCTCAGATCAGCTATATCTTAAGTAAATCTATGAAACCTTACACCCCAAGCA 2280
Oy 672 ProProThrLeuSerThrAspHlsThrSerThrGlyTyrrValTPAlaGlyGluLeu 691
Db 2281 -----AAGGAGAGAGCTGTGTATTAATGACGTTGCTGGAATTT 2325
Oy 692 GlyThrArgValAlaValGluAsnthrSerGlyArgGlyPhePheGlnTyrrThrPro 711
Db 2326 GCGAGCTCCCAACACACATGCTTTAAGCATAGAGGCTCTTCCAGCGCTATTTCT 2385
Oy 712 PheVallyleValGlnAlaValTyrrAlaArgGlnAspSerPheValGluLeuGly---Ala 730
Db 2386 TTCACTCAAGATGAGAGCTCTTACATACACCAATATGCTTCAAGAACGTAACTAAC 2445
Oy 731 lleserAlaspPheSerAspSerhiseryrAsnleuAlaileProleuGlylylelys 750
Db 2446 TTGGTACGATCTTTCGATGAGCGGTGATTTAATTAACGCTCTGCGCTATGGAATTA 2505
Oy 751 LeuGluLys-----ArgPheAlagluGlnTyrrHlsValAlaMetTyrrSerPro 768
Db 2506 TTCAGAGATTCGAGAAACGAGCGTGCCTTACGAACTAGTCATAGCTTACC 2565
Oy 769 AspValCysArgSerAsnProLysCysThrThrThrleuLeuSerAsnGlnlySerTyr 788
Db 2566 GATGTCTATCGTAAGATTCCTGACTGCACGACGCTCTCTCAATCAACAATACCTCGTG 2625
Oy 789 LysThrlyGlySerAsnleuAlaArgGlnAlaglylyleValGlnAlaSerGlyPheArg 808
Db 2626 AAACCTACAGAGAAATCTTCAAGACAGCTGTATCGAAGAGCAGGATCTTTAT 2685
Oy 809 SerLeuGlyAlaAlaAlagluLeuPheGlyAsnPhelGlyPheGluTyrArglySerSer 828
Db 2686 GCCTTCTCCAAATCTTGAAGGTCAACAAGTAACTATCTAGAAATTCGTGATCTTCA 2745
Oy 829 ArgSerTyrrAsnValaspAlaglySerlylylelysphe 841
Db 2746 CGCAGCTAACATGCAATCTTGAAGGTAAAGTTCCAGATTG 2784

RESULT 10
US-10-289-762-1/c
; Sequence 1, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Grifols, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCES: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289, 762
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae

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LOCATION: (540001)..(555000)
 OTHER INFORMATION: n=a or c or g or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (555001)..(570000)
 OTHER INFORMATION: n=a or c or g or t
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 NAME/KEY: misc feature
 LOCATION: (570001)..(585000)
 OTHER INFORMATION: n=a or c or g or t
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 NAME/KEY: misc feature
 LOCATION: (585001)..(600000)
 OTHER INFORMATION: n=a or c or g or t
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 LOCATION: (600001)..(615000)
 OTHER INFORMATION: n=a or c or g or t
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 NAME/KEY: misc feature
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 NAME/KEY: misc feature
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 OTHER INFORMATION: n=a or c or g or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (660001)..(675000)
 OTHER INFORMATION: n=a or c or g or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (675001)..(690000)
 OTHER INFORMATION: n=a or c or g or t
 FEATURE:

Alignment Scores:

Pred. No.: 1,72e-125 Length: 1230025
 Score: 1365.00 Matches: 329
 Percent Similarity: 51.04% Conservative: 161
 Best Local Similarity: 34.27% Mismatches: 320
 Query Match: 31.78% Indels: 151
 Gaps: 22

US-09-830-446-27 (1-841) x US-10-289-762-1 (1-1230025)

1 MetlyslleProleuArpHeuleule---SerleuValProthreleuSerMetSer 19
 518200 ATGAAATGCCATTTTCCGTAGCTCTCTGCAATTCGCAATGTTTACTGTTGT 518141
 20 AenleuleuglyAlaAlaThrgIuLeuSerAlaSerAsnSerPheAspGlyThr 39
 518140 TCCACTGTTTTCGCAACTCTGAAATATATAGCCCTCTGATAGCTTTGACGAAGT 518081
 40 ThiserThrSerPheSerSerlyThrSerSerAlaThraSpGlyThrAsnYrVal 59
 518080 ACTAACACAGGACCTATACCTCTTAA-----AATACGACTCTGAAATAGACTATACT 518027
 60 PheLyAspSerValValIleGluAsnValProlyThrGlyIuThrgInSerThrSer 79
 518026 CTGACAGGAGATATACTCTGAAAACCTT-----GGGATTCGCGACCTTTAACG 517976
 80 -----CyPheLyAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyPhe 97
 517975 AAGGCTGTTTTCGACACTACGAGATCT-----TTAAGCTTGGCGGTAAAGGGTAC 517922
 98 SerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGlu 117
 517921 TCACTTCTTTTAAAT---ATMAAGTCTAGCTGAAGGCGCAAA-CTT---TCTGTT 517869

118 AlaAlaAsnlyThrValThreSerGlyPheSerAlaLeuSerPheLeuSerPro 137
 517868 ACAACTGATTAATAATCTGCTCTACAGAGATTTTCGAGTTACTTCTTAGCGGCCCA 517809
 138 AlaSerThrValThr----- 142
 517808 TCATCGTAAATCAACACCCTCAGAAAAGTGCAGTTAATGTGAGGGATCTTACA 517749
 143 -----AenglyY-Leu----- 145
 517748 TTTGATACAAATGAACTATTATTAAACAGATTACTGTGAGAAAATGCGGACAT 517689
 145 ----- 145
 517688 TTCTACCAAAATCTTCTTTGAAAAACAGCAGGATTCATTTCTTTGAAAGGAATTA 517629
 145 ----- 145
 517628 ATCGAGCGCAACAGGAAAAAGTGGGCTATTGTGCTACTGTAATATTAC 517569
 146 -----GlyAlaAla 148
 517568 AATATATCGGCTCTACCTCTTCTGCAACATATTGCTGAAGCTGAGGTGAGCTAT 517509
 148 eAsnVallysglyAsnleuSerleuLeuAspAsnAspIyValleuIleGlnAspAsnph 168
 517508 AATATGACACAGAAATCTGATCAATTACAGGAAATACGCTCTGTATTTCTGAAAAATAG 517449
 168 eSerThr-----GlyAspGlyGlyAlaIleAsnCyAlaGlySerleuysIleAla 185
 517448 TGTGACAGCGACCGCAGAAATGAGAGGCTCTTCTGAGATCCGATGTACCAATTC 517389
 185 AAsnAsnlySerleuSerPheIleGlyAsnSerSerThrArGlyGlyAlaIleAla 205
 517388 TGGAAATACAGATGATATTCTCTGAGAAACCAAGCTTACTATAAGCGGAGCATTTA 517329
 205 sThrLyAsnleuThrleuSerSer-----GlyGlyGlyIuThreuphe-GlnglyA 222
 517328 TGTATAGAAAGCTTACACTGCTCCGGGGGGGGGGGTATCTCTTTCTTAACAATA 517269
 222 snThrAlaProThrAlaAlaGlyLyserGlyAlaIleAlaIleAlaAspSerGlyThrL 242
 517268 TAGTCCAAAGTACCACTGACAGATATAGTGAAGCATTTCTATCTGCGACGTGAGAGT 517209
 242 euserIleSerGlyAspSerGlyAspIleIlePheGlyGlyAsnThrIleGlyAlaThr- 261
 517208 GTAGCTTTACAGCAAGACAGGAGACATTACTCAATGGAATGCCATTGTGCACTA 517149
 262 -----GlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaIleThrAlaL 280
 517148 CACCACAAATACGAAAAGAAATCTATTGACATGATCTACTGCAAAAGATACAGAAAT 517089
 280 euaIrgAlaIleGlyGlyHisThrIleIyrrPheYrAspProIleThrValThrgIySert 300
 517088 TACGGCAATATCTGGGATATGACATCTTTCTAGATCCATTAATCTCTAATACGGCTG 517029
 300 hrSerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnlysglyYrT 320
 517028 CGGATTCACAGATTAATCTTAATCTCAATAGCGTATGAGTAATGACTACAGATTATA 516969
 320 hrGlyThrIleValPheSerGlyGlyIuLyLeuThrgIuAlaGlyAlaIleAspGlyIuYsA 340
 516968 GTGGGTGATTTGTTTCTGCTGTAAGAGCTCTGGAAGATGAAGCAAAAGTTGCAGACA 516909
 340 snArGThrSerlyleuLeuGlnIleAsnValAlaPheLyAsnGlyYrThrValIleuLyvg 360
 516908 ACCTCACTTCAACGCTGAAGAGCCTGTAAGCTTAACTGACAGAAATTTAGATTAAAC 516849
 360 lyAspValIleuSerAlaenglyPheSerGlnAspAlaAsnSerlySerleuIleMetA 380
 516848 GTGGGTGACTCTGATACGAAGAGCTTTACTACAGACCGCGGTTCTCTGTATATTAGG 516789

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QY 380 epLeuGlyTherSerLeuValAlaLeuThrGluSerIleGluLeuThraLeuGluIleA 400
DB 516788 AGCGGCGCAACGTTAAAGAAAGTACAGAGGAGGACCTTAAACAGGCTTTCCATTC 516729
QY 400 enLeaSerSerLeuThraenGlyLysLeuValIleLeuSerSerAlaAlaThrAlaGluIleA 420
DB 516728 CTGTAAGACTCTTAAAGCGGAGGAGTAAAGAAAGTTGAATTCCTGCTTTCGACGAAAGTAAA 516669
QY 420 epLeaGlyLeaPArgProValAlaLeuAlaIleSerArgProLeuSerPheTyrgLinaenG 440
DB 516668 AGTGAAGCCTTAAGTGTGCTCCGATTCCTTTGGATTAACCAAGGAATGCTTTGAAATTC 516609
QY 440 lypheLeuAnGlyLysPheHiseTyraPArgLyIleLeuGluLeuPheAlaGlyLysAapI 460
DB 516608 AGCAAGTAAAGAAACTCAAGACTT---TCATTTGTGACAGCTCTGCT---CTGGGTA 516555
QY 460 lvalIleSerAlaSerSerArgSerIleAapAlaAlaGluSerPro-----TyrgLyT 478
DB 516554 CTGCAACAACTAACAGATGTTCCAGCGGTTCTTACAGTACCAACTCTTACGCACTATGGGT 516495
QY 478 yrgLingLyLysTyrrThrIleAenTyrrSerThraP-----AapLyL 492
DB 516494 ATCAAGTACTTGGGAATGACTGGGTGATGATACCCGACAGACTCCAAAGACTTAAGA 516435
QY 492 yvalIleThraIleSerThraAlaLysGluSerPheAanProThraIaGluGluIleAProL 512
DB 516434 CAGCGACATTAAGTTCGACCAATAACGCGCTACCTTCGATCCGATCCGATCCGACGACTT 516375
QY 512 euValProAenLeuLeuThrGlySerPheIleAapValArgSerPheGluAanPheIleG 532
DB 516374 TAGTTCCTTAATAGCTTGGGATCTTTTTCAGACATCCAAAGGATTCAGAGGTGCATAG 516315
QY 532 luleuGlyThrGluGlyAlaProTyrgLysLysPheThraIaGlyIleSerAanV 552
DB 516314 AAGAAGAGCTTGAAGCTTGTGTGATGATGAGGCTTGGGGTGGCGAGTCCGCAATT 516255
QY 552 alleuHiseArgSerGlyArgGluAenGluArgLysPheAanGlyIleSerGlyAlaVal 572
DB 516254 TCTTAAGATAAGTAAGTAAGAAAGGGAAGAAAGCAAAATCCGTCAATATGCGTGATAG 516195
QY 572 aIvalGlyLaseThraGlyMetProGlyLysAanThraLeuSerLeuGlyPheAlaGluL 592
DB 516194 CTATCGAGAGTCAAGGCAAACTTGTTCGAAAACTTAATTAAGCTTGGCTTTGGCAAC 516135
QY 592 euPheAlaArgPheLysAapTyrgPheMetAanThraAanPheAlaLysThraIaGlyLys 612
DB 516134 TCTTTGGTACGCAATTAAGATTTCTTAAGTCAAAATTAAGTCAATGATCACTATGCGAGAG 516075
QY 612 exLeuArgLeuGluIleAapAlaSerLeuTyrrSerValIleSerIleLeuGlyLysG 632
DB 516074 CCTTCAATATCCAAACATTAAGATTAAGTGGTTCATAGGTTGTCTTTAATTAAGTAA- 516016
QY 632 lylGlyLeuArgGluIleLeuLeuProTyrrValIleTyrrLeuProCysSerPheTyrg 652
DB 516015 -----CTTCCGCGCTTGGAGTCAATAAACCCCTCGTTTGAAG 515976
QY 652 lylGluLeuSerTyrgLysIleThraPheIleArgMetLysThraGluSerLysProPheP 672
DB 515975 GCGAGGCTCCTTAAGCCAGCGTCAATTAAGTCAAGAAAGAAAGTACTGCGGTATCTG 515916
QY 672 roProThraLeuSerThraPheIleThraSerTyrgLyLysTyrrValIleThraIaGlyLysG 692
DB 515915 AAGGTG-----AAAGTCTTGGGGAATTAAGCTTTTAACATGATGTTGG 515871
QY 692 lYThraArgValAlaValGluAanThraSerGlyArgGlyPhe-----P 706
DB 515870 GA-----GCTTCTTCAATCTTAATCTTAATCTTAATCTTAATCTTAATCTTAATCTT 515832
QY 706 heGluGluTyrrThraProPheValLysValGluAlaValTyrrAlaArgGluAanSerPheV 726
DB 515831 TTGATACCTTAAGTCAATTAAGTCAATTAAGTCAATTAAGTCAATTAAGTCAATTAAGTCA 515772
QY 726 aIgluLeuGlyAlaIleSerArgPheSerAanPheSerHiseTyrrAanLeuAlaIleP 746

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DB 515771 CGGAAAGAGTACAGAGAGAGATCTTTGATGACAGCAACCTTCATTTATCTTGC 515712
QY 746 roLeuGlyLysLeuGluLysArgPheAla-----GluGluTyrrThraIleValV 763
DB 515711 CTATAGGGGTGAAGTTTGAGAG---TTCTGATTTGATATAGACTTTTCTTATGATCTGA 515655
QY 763 aIAlaMetTyrrSerProAapValCysArgSerAanProLysCysThraThraLeuLeuS 783
DB 515654 CTTATTCATGATTTCTGATCTTATCCGCAATGATCCAAATGCACTACAGACCTTGTA 515595
QY 783 eThraGluGlySerTyrrThraLysGlySerAanLeuAlaArgGluAlaGlyIleValG 803
DB 515594 TCAGCGGAGCCTCTTGGGAACCTTAATGCCAATACCTTAAGCCAGACAGCGCTTGAAGTGC 515535
QY 803 lnaIleSerGlyPheArgSerLeuGlyAlaAlaGluLeuPheGlyAanPheGlyPheG 823
DB 515534 GTGACAGGACGTACTACAGCCTTCTCTCTATGTTGAAGTGTCCGACGATTTGCTTTG 515475
QY 823 lUTTPArgGlySerSerArgSerTyrrAanValAapAlaGlySerLysIleLysPhe 841
DB 515474 AAGTGTGTGATCTCAAGGATTTAATGATGATCTTGGGGTAAAGTCCAAATTC 515419
RESULT 11
US-10-312-273-20
; Sequence 20, Application US/10312273
; Publication No. US20040005667A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035MO
; CURRENT APPLICATION NUMBER: US/10/312,273
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 20
; LENGTH: 2241
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-20
Alignment Scores:
Pred. No.: 5,716-129 Length: 2241
Score: 1357.50 Matches: 330
Percent Similarity: 56.17% Conservative: 116
Best Local Similarity: 41.56% Mismatches: 270
Query Match: 31.61% Indels: 78
DB: 12 Gaps: 21
US-09-830-446-27 (1-841) x US-10-312-273-20 (1-2241)
QY 75 ThrGlnSerThraSerCysPheLysAanPheAla-----AlaAlaGlyAapLeuAanPhe 92
DB 16 TTGAAATACCTCTTCAAGAAAGGCGGAGCATTAAGACTTCCGATGCTTACCAT 75
QY 93 leuGlyGlyGlyPheSerPheThraPheSerAanIleAapAlaThraThraIaSerGlyAla 112

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QY 810 LeuGLYAlAlAlaGLLeuPheGLYAsnPhcGLYThrPArgGLYSerSerArg 829
 DB 2143 TTTAACTTCAATTTTAAAGCTTTAGCCAAATTTCTTTGAAATTCGCGTCACTCGC 2202
 QY 830 SerTYrAsnValAspAlaGLYSerLYSGLYLeuPhe 841
 DB 2203 AATTACAAATGTAGACTTAGAGCAAAATACCAATTC 2238
 RESULT 12
 US-10-312-273-154
 / Sequence 154, Application US/10312273
 / Publication No. US20040005667A1
 / GENERAL INFORMATION:
 / APPLICANT: CHIRON SPA
 / TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
 / FILE REFERENCE: P025035WO
 / CURRENT APPLICATION NUMBER: US/10/312.273
 / CURRENT FILING DATE: 2002-12-20
 / PRIOR APPLICATION NUMBER: 0016363.4
 / PRIOR FILING DATE: 2000-07-03
 / PRIOR APPLICATION NUMBER: 0017047.2
 / PRIOR FILING DATE: 2000-07-11
 / PRIOR APPLICATION NUMBER: 0017983.8
 / PRIOR FILING DATE: 2000-07-21
 / PRIOR APPLICATION NUMBER: 0019368.0
 / PRIOR FILING DATE: 2000-08-07
 / PRIOR APPLICATION NUMBER: 0020440.4
 / PRIOR FILING DATE: 2000-08-18
 / PRIOR APPLICATION NUMBER: 0022583.9
 / PRIOR FILING DATE: 2000-09-14
 / PRIOR APPLICATION NUMBER: 0027549.5
 / PRIOR FILING DATE: 2000-11-10
 / PRIOR APPLICATION NUMBER: 0031706.5
 / PRIOR FILING DATE: 2000-12-22
 / NUMBER OF SEQ ID NOS: 664
 / SOFTWARE: SeqMan9, version 1.02
 / SEQ ID NO 154
 / LENGTH: 2811
 / TYPE: DNA
 / ORGANISM: Chlamydia pneumoniae
 US-10-312-273-154
 Alignment Scores:
 Pred. No.: 1,486-126 Length: 2811
 Score: 1335.50 Matches: 311
 Percent Similarity: 49.26% Conservative: 157
 Best Local Similarity: 32.74% Mismatches: 359
 Query Match: 31.09% Indels: 123
 DB: 12 Gaps: 14
 US-09-830-446-27 (1-841) x US-10-312-273-154 (1-2811)
 QY 1 MetLYIleProLeuArGpHeLeuLleSerLeuValProThrLeuSerMetSerAan 20
 DB 1 AATGAATCTCTGCTCTCTGTTGTTCTTTCTTCAATCCGCTCTTTCATGCTCTCT 60
 QY 21 LeuLeuGLYAlAlAlaThrGLuGLuLeuSerLAsnSerPheAspGLYThrThr 40
 DB 61 ATAGTCGGCGAGAGGTGACCTTAGAT--AGCAGCAATATATGCTATATGATGATCTAAC 117
 QY 41 SerThrThrSerPheSerSerLYSThrSerSerAlaThrAspGLYThrAsnTYrValPhe 60
 DB 118 GGAACCTACCTTACCGCTTTTCCACTACGACGCTCTCGCAGAACTACCTATTCCTTA 177
 QY 61 LysAspSerValValIleGLuAsnValProLYSThrGLYGLuThrGLuSerThrSerCys 80
 DB 178 CTTTCCGACTATCTCTTCAAAATGCGAGGCTTAGAAATCCCTTAGCCTCAGGATGC 237
 QY 81 PheLYAsnAspAlAlAlaGLYAspLeuAsnPhcLeuGLYGLYLYPheSerPheThr 100
 DB 238 TTCTTGAAG--CGCGGCGCGAGATCTTATCTTCCAAAGAAATCAACATGCACTGAAG 291
 QY 101 PheSerAsnIleAspAlaThrThrAlaSerGLYAlAlAlIleGLYSerGLuAlAlaAsn 120

DB 292 TTTCATTTATCAATCGCGGCTCTACCGCTGGAACCTGAGCACTACCTACGACAGAT 351
 QY 121 LysThrValThrLeuSerGLYPheSerAlaLeuSerPheLeuLYSerProIAsnThr 140
 DB 352 AAGAAATCTTCTCTTATATATTTTCTTGAACCTCTTATATTAATCTTGTCTCTCTTT 411
 QY 141 ValThr--AsnGLYLeuGLYAlAlaAsnValLYGLYAsnLeuSerLeuAspAsn 159
 DB 412 CTCTCTCTACCTGACAAATGCTTTAAATCTGTGGGAATATATCTTACTGCAAT 471
 QY 160 AspLYValLeuIleGLuAsnPhcSerThrGLYAspGLYAlAlaIleAsn 177
 DB 472 TCCCAATATATATTACTCAGAACTCTCTCGATATACGCGGCTGTATCATATAGAA 531
 QY 177 ----- 177
 DB 532 AACTTTATATATACGAGACATCTCAGTTGGAGCTTTTCGAAACCAAGCCTTCACA 591
 QY 178 -----CysAlaGLYSerLeuLYIleAlaAsn----- 186
 DB 592 GGGAGCAAGGGGTGTAGTTAGCTACAGAACTATATCTATTCAGAACCCCTGG 651
 QY 186 ----- 186
 DB 652 ATAGTTCTCTCTCAAAACCTAGCGAAAGATCTGGCGTCTGTACAGACTGAC 711
 QY 186 ----- 186
 DB 712 AACTGTGATTACAGATTAATTCAAGTATCTTTCAGCGCAATATGCTTGGAGACC 771
 QY 186 ----- 186
 DB 772 GCTCAAGCTCAGGGCGGGCTATTTGTCACATACAGATTAACAGTACTTACT 831
 QY 187 ---AsnLYSerLeuSerPheIleGLYAsnSerSerThrArgGLYAlAlaIleAsn 205
 DB 832 GGGACCAAAACCTCTTTCACAAATATATACGATTCACATATGCGGAGCATCTCT 891
 QY 206 ThrLYAsnLeuThrLeuSerSerGLYGLYGLuThrLeuPheGLYAsnThrAlaPro 225
 DB 892 GGACTCAAGTCAAGATATTCCTCGAGGCTCTACTCTTTCAAAGTATATCTCAGGA 951
 QY 226 ThrAlaAlaGLYAsn-----GLYGLYAlAlaIleAlaAspSerGLYThrLeuSer 243
 DB 952 AGTAGCGCGGTCAAGGAGAGAGAGATCAATATATGCAATCTGCTGGAATCTCGT 1011
 QY 244 ILeSerGLYAspSerGLYAspIleIlePheGLYAsnThrIleGLYAlaThrGLYThr 263
 DB 1012 CTCTCTGCTACTTGTGAGATATTAACCTTCATATACAAACCAAGTACCAAGGAGACAA 1071
 QY 264 ValSerPheSerAlAlaLeuLeuGLYThrSerAlaLYSGLYThrAlaLeuAla 283
 DB 1072 AGTACAGAAAGCAATATATATATGATTCACCGCTTAAGTCAATCGATACAGCTGCT 1131
 QY 284 GLuGLYIleThrIleTYrPheTYrAspProIleThrValThrGLYSerThrSerValAla 303
 DB 1132 ACGGGCAATCTATCTATTTATATGATCCATACCAATTCAGAAACCCGAGCTTAC 1191
 QY 304 AspAlaLeuAsnIleAsnSerProAspThrGLYAspAsnLYSGLYTYrThrGLYThrIle 323
 DB 1192 GACACTTGAATTAATTAATTAAGATGCAAGTCAAGATGAGATGGGGTGCAT 1251
 QY 324 ValPheSerGLYGLYLYLeuThrGLuAlaGLYAlaLYSAspGLYLYSAsnArgThrSer 343
 DB 1252 GTCTTTTCTGAGAAAGCTTTCCTTACAGAAAGCAATGCTGCAACCTCACTCT 1311
 QY 344 LysLeuLeuGLuAsnValAlaPheLYSAsnGLYThrValValLeuLYSGLYAspValVal 363
 DB 1312 ACTATTCGACAACTGCACTATTAGCGCGGAGATCTTGTACTCTGTATGAGATGACC 1371
 QY 364 LeuSerAlaAsnGLYPheSerGLuAspAlaAsnSerLYSLeuIleMetAspLeuGLYThr 383

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Db      1372 GTAACCTTCAGAGATCTGACATCAAGTCCAGATCCCGCATCTTAATGATGCGGAGACT 1431
Qy      384 SerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSer 403
Db      1432 ACACTTAGTGTAAAGAGCAATCTTCGCTTAATGCGCTTAAGCATTAATCTCTCTCT 1491
Qy      404 LeuArgAsnGlyLysLeuIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArgIle 423
Db      1492 TTAGATGGAACCAACAGGACAGCTTTAAACAGAAAGCTGCAGATTAATAATTCAGCCCA 1551
Qy      424 AspArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeuAsn 443
Db      1552 TCGGAGACCATTCGCTTATTTGACACGGAAGGCTCATCTTAAGAGATCATTAATTAATA 1611
Qy      444 GluAspHisLeuSerTyrAspGlyLysLeuGluLeu---AspAlaGlyLysAspIleValIle 462
Db      1612 AGTGTAGTACTATCTCT---CTTCTGAACCTTACACCGCAGAGACCAACGAAAGAT 1668
Qy      463 SerAlaAspSerArgSerIleAspAlaValGlnSerPro-----TyrGlyTyrGln 479
Db      1669 ACTCTGGAGAGCTCTTCTACCTGACTCTTCAAGAACCTGAAACCACTACGGGATTCACA 1728
Qy      480 GlyLysTyrThrIleAsnTyr-----SerThrAspAspLysLysValaThrValSerTyr 497
Db      1729 GGAAACTGGCAGATGTGCTTGGCGCAATGCAACTCTCAAAATAAGGAAGCATCACTGG 1788
Qy      498 AlaLysGlnSerPheAsnProThrAlaGlnGlnGluValProLeuValProAsnLeuLeu 517
Db      1789 ACCCGTACAGATACATCTTCTAGTCTCTGAGAGAAAAGTAATCTCTCTTAATAGCTTA 1848
Qy      518 TTPGlySerPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGly 537
Db      1849 TGGGAAACTTTATAGATATACCTGATCATCATCAGCTTAATGAAACCAAGTCCAGTGG 1908
Qy      538 AlaProTyrGlnLysArgPheTyrValAlaGlyIleSerAsnValLeuHisArgSerGly 557
Db      1909 GAGCTTTTGAACGCTGATGCTATGCGCTTCAAGAAATTTCTCTATAGAGATCTCT 1968
Qy      556 ArgGluAsnGlnArgLysPheArgHisValSerGlyAlaValAlaGlyLysSerThr 577
Db      1969 ATGCCACCGCGCAGATGTTCCGCAATATCAGCGGCGGTTATGCACTAGAGATCAACAGA 2028
Qy      578 ArgMetProGlyLysAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLys 597
Db      2029 ACAACCTCCGCGAGATCAGCTTACTTTGCTTTCGCAAGCTCTTCTGAGATGCC 2088
Qy      598 AspTyrPheMetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHis 617
Db      2089 AATCATATATTACAGTAAAGAACCAACGAGATACTTACGGTGCCTTTGTATTCCACCAT 2148
Qy      618 AspAlaSerLeuTyrSerValValSerIleLeuLeuGlyGluGlyLysLeuArgGluIle 637
Db      2149 ACAAGAGGCTCTTCAGCATCCGCCAATTTCTCTGGGAGAAACCAACCGAGCTCCCTGG 2208
Qy      638 LeuLeuProTyrValSerLysThrLeuProCysSerPheTyrGlyLysLeuSerTyrGly 657
Db      2209 GTGCTCTCGAGATCTCCAGATCATCTTATCTTGATGAGTAAATTCAGTATCTTC 2268
Qy      658 HisThrAspHisArgMetLysThrGluSerLeuProProProProThrLeuSerThr 677
Db      2269 CATACAGACCAACCAATGAAG-----ACATATTATATACC 2301
Qy      678 AspHisLeuThr-----SerTyrGlyLysTyrValThrAlaGlyLysLeuGlyThr 693
Db      2302 GATTAATCTATCATCAAGGCTCTTGAAGAAACGATGCTCTGTCGCAATCTTGAGCT 2361
Qy      694 ArgValAlaValAlaGluAsnThrSerGlyArgGlyPhePheGlnGluTyrThrProPheVal 713
Db      2362 AGCGTGCCTTTGTT---ATTTCGTTCCGTAATCTCTGAAGAAATTCAGACCTTTTGTTC 2418
Qy      714 LysValGlnAlaValAlaGlyLysAspSerPheValGluLeuGlyAlaIleSerArg 733
Db      2419 AAAGTACAGTATATCTATGCGCATGCAAGACTTCTACAGCGCTCATGCTGAAGAGCC 2478

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Qy      724 AspSerAspSerHisLeuTyrAsnLeuAlaIleProLeuGlyLysLeuGluLys 753
Db      2479 GCTTTCATTAAGAGCACTTATCACTAGAGATCTCTATAGCGTCACTTCAAGAA 2538
Qy      754 -----ArgPheAlaGluGlnTyrThrHisValAlaAlaMetTyrSerProAspValCys 771
Db      2539 GACTCAAAATGCAAAAGGAAGCAATCAGATCTTACTCTTATGATATATCTGATCTTAC 2598
Qy      772 ArgSerAsnProLysCysThrThrThrLeuLeuSerAsnGlnGlySerTyrThrLys 791
Db      2599 CGACCAATCTCTTAATGCAAACTTCCCTAATAGCTACGATGCTACACTGATGCGCTAT 2658
Qy      792 GlySerAsnLeuAlaArgGlnAlaGlyLysLeuGlnAlaSerGlyPheArgSerLeuGly 811
Db      2659 GGTACCAACCTCGACGACGACAGCTTTTCTGCTGCTGCGAACCATTTCCAGTGAAC 2718
Qy      812 AlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTyrArgLysSerArgSerTyr 831
Db      2719 CCCCAATGGAATCTTGGTCAATTCGCTTTGAAAGTACGAAGTCTTCAAGAAATAT 2778
Qy      832 AsnValAspAlaGlySerLysIleLysPhe 841
Db      2779 AATACAAACCTAGGCTCTAAGTTTGTTC 2808

RESULT 13
US-09-452-380-1
/ Sequence 1, Application US/09452380
/ Patent No. US2002009340A1
/ GENERAL INFORMATION:
/ APPLICANT: MURDIN, Andrew D.
/ APPLICANT: WOMEN, Raymond P.
/ APPLICANT: WANG, Joe
/ APPLICANT: DURN, Pamela
/ TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
/ FILE REFERENCE: US 032931/0216
/ CURRENT APPLICATION NUMBER: US/09/452,380
/ PRIOR FILING DATE: 1999-12-01
/ PRIOR APPLICATION NUMBER: US 60/132,272
/ PRIOR FILING DATE: 1999-05-03
/ PRIOR APPLICATION NUMBER: US 60/113,439
/ PRIOR FILING DATE: 1998-12-01
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 3050
/ TYPE: DNA
/ ORGANISM: Chlamydia pneumoniae
/ FEATURES:
/ NAME/KEY: CDS
/ LOCATION: (101)..(2908)
US-09-452-380-1

Alignment Scores:
Pred. No.: 1,68e-126 Length: 3050
Score: 1335.50 Matches: 312
Percent Similarity: 49.26% Conservative: 157
Best Local Similarity: 32.74% Mismatches: 359
Query Match: 31.09% Indels: 123
DB: 9 Gaps: 14

US-09-830-446-27 (1-841) x US-09-452-380-1 (1-3050)
Qy      1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
Db      101 ATGAAGTCTCTGCTGCTCTGTTGTTCTTTCTTCAATCCCGCTTTTTCATCGCTCTCT 160
Qy      21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40
Db      161 ATAGTGGGCGGACAGATGACCTTAGAT---AGCGCAATTAATAGCTATGATGATCTAAC 217
Qy      41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60

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Db      218 GGAACCTACCTTCAAGGCTTTTCCACTACGACGCTGCTCAGAACTACCTTCTTCTTA 277
Qy      61 LysAspSerValValIleGluAsnValProLysThrGlyLysThrGlnSerThrSerCys 80
Db      278 CTTTCCGACCTATCTTCAAAATGCGAGGCGCTTAGAAATCCCTTAGCTCAGATGC 337
Qy      81 PheLysAsnAspAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThr 100
Db      338 TTCTCTGAAG-----GGGGGCGGCGATCTTATCTTCAGAGAAATCAACATGACGAG 391
Qy      101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGlyAlaAlaAsn 120
Db      392 TTTCAGTTATCAATGCGGCTCTAGCGCTGAGACTGACCTGACCTCAGACGACGAT 451
Qy      121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProLysThr 140
Db      452 AGAATCTCTCTTATATGATTTTCTAGACTCTCTATTTATCTCTTCTCTCTCTTCTT 511
Qy      141 ValThr---AsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuAspAsn 159
Db      512 CTCTCTCTCTACGACAAATGCTTTAAATCTGTGGGAAATCTATCTTAACCTGGAAAT 571
Qy      160 AspLysValLeuIleGlnAspAsnPheSerThrGlyAspGlyAlaAlaAsn----- 177
Db      572 TCCCAATATATATTTACTCAAGAACTCTCGTCAATTAACGCGGTGTATCAATACGAA 631
Qy      177 ----- 177
Db      632 AACTTCTTATTATCAGGACATCTCAGTTGCGAGCTTTGAGAAACCAAGCTTCA 691
Qy      178 -----CysAlaGlySerLeuLysIleAlaAsn----- 186
Db      692 GCGAAGCAAGCGGTGTATGTTACGCTACAGAACTATATCTATCGAAGACAGCCCTGG 751
Qy      186 ----- 186
Db      752 ATAGTTCTTCTCTCAAAACCTAGCGAAAGATCTGCGGTCTCTGTACACACTGAC 811
Qy      186 ----- 186
Db      812 AACTGTTCAATTACAGATTAATTCAAGTATCTTTGACGCAATAGTCTTGGAAAGCC 871
Qy      186 ----- 186
Db      872 GCTCAAGCTCAAGGCGGCGCTATTTGTGACTACGACAGATTAACAGTACCTTACT 931
Qy      187 ---AsnLysSerLeuSerPheIleGlyAsnSerSerThrArgGlyAlaIleHis 205
Db      932 GCGAACAACCACTCTCTTCAACAAATATATACAGATTAATGCGGAGCCATCTCT 991
Qy      206 ThrLysAsnLeuThrLeuSerSerGlyGlyLysThrLeuPheGlnGlyAsnThrAlaPro 225
Db      992 GGACTCAAGGCTCAATATTTCCGAGAGTCTACTCTATTTCAAAAGTAAATATCTCAG 1051
Qy      226 ThrAlaAlaGlyLys-----GlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSer 243
Db      1052 AGTAGGCGCGCTCAGGAGAGAGAGAGAGATCAATATACATCTGCTGGAGAACTCGCT 1111
Qy      244 LLeSerGlyAspSerGlyAspIleIlePheGlnGlyAsnThrIleGlyAlaThrGlyThr 263
Db      1112 CTCTCTGCTACTCTGAGATATATTAATCTCAATTAACCAACAGTACCAACGAGAGACA 1171
Qy      264 ValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuAlaAla 283
Db      1172 AGTACAGAAACGCAATATATATCATTTGATATACGCTTAAGTCACTGATCAACAGCTGC 1231
Qy      284 GlnGlyHisThrIleThrPheThrAspProIleThrValThrGlySerThrSerValAla 303
Db      1232 ACCGGGCAATCTATCTATTTCTATGATCCATCAACAAATCCAGAACCGAGCTTCAAC 1291
Qy      304 AspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGlyLysThrGlyThrIle 323

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Db      1292 GACACATTGAATTAACCTTAGCAGATGCGAACAGTGAATGAGTGGGGTGGCATT 1351
Qy      324 ValPheSerGlyLysLysLeuThrGlyAlaGlyAlaLysAspGlyLysAsnArgThrSer 343
Db      1352 GTCTTTTCTGGAGAAAGCTTTCCCTACAGAAAGCAATGCTGCAACGTCACCTCT 1411
Qy      344 LysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspValAla 363
Db      1412 ACTATCCGACCACTTCAGATATTAGCGCGGAGACTTGTACTTCTGATGAGATCCACC 1471
Qy      364 LeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleLysAspLeuGlyThr 383
Db      1472 GTATCTTCAAGAGATCTGACTCAAACTCAGATCCCGGATCTTAATGATGGGGGACT 1531
Qy      384 SerLeuValAlaAsnThrGlnSerIleGlnLeuThrAsnLeuGlnLysAsnIleAspSer 403
Db      1532 ACACCTTAGTCTTAAGAGCAATCTTTGGCTTAATGCGCTTAGACATTAATCTCTCTCT 1591
Qy      404 LeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArgIle 423
Db      1592 TTATGATGAACCAACAGGCGAGCTTTAAACAGAACTGACAGATTAATAATCAACCTTA 1651
Qy      424 AspArgProValValLeuAlaIleSerAspGlnSerPheThrGlnAsnGlyPheLeuAsn 443
Db      1652 TCGGAACGATGCGCTTATTTGACAGGAAGGCTCATTTATGAGAAATCAATTAATAAA 1711
Qy      444 GluAspHisSerThrAspGlyLysLeuGlnLeu---AspAlaGlyLysAspIleValIle 462
Db      1712 AGTCTAGTACCTATCTCT---CTTCTGAATTTACCAACCGGAGAGCCAAAGGAAAT 1768
Qy      463 SerAlaAspSerArgSerIleAspAlaValGlnSerPro-----TyrGlyTyrGln 479
Db      1769 ACTCTGAGAGCTCTTCTTCAACCTGACTCTTCAAGAACCTGAACCCAGATGAGGTATCAA 1828
Qy      480 GlyLysTyrThrIleAsnTyrP-----SerThrAspAspLysLysAlaThrValSerTyr 497
Db      1829 GGAACCTGGCAAGTGTCTTGGGCAATGCAACATCTCAAAATATAGAAACATCAACTGG 1888
Qy      498 AlaLysGlnSerPheAsnProThrAlaGlnGlnAlaProLeuValProAsnLeuLeu 517
Db      1889 ACCGTTACAGATACATTCCTAGTCTCTGAGAGAAAGTAAATATCTCTTAATATAGCTTA 1948
Qy      518 TyrGlySerPheIleAspValArgSerPheGlnAsnPheIleGlnLeuGlyThrGlnGly 537
Db      1949 TGGGGAACCTTATATAGATATAGCTGATCAATCACTTATAGAAACCAAGTCCAGTGG 2008
Qy      538 AlaProTyrGlyLysArgPheThrPValAlaGlyLysSerAsnValLeuHisArgSerGly 557
Db      2009 GAGCTTTTGAAGCGTATGAGCTATGCTTTCAGGAATGCGCAATTTCTTATATAGAGATTCT 2068
Qy      558 ArgGluAsnGlnArgLysPheArgHisValSerGlyAlaValAlaGlyAlaSerThr 577
Db      2069 ATGCCACCGCGCATGCTTTCGCAATATCGAGGAGGAGTTATGACCTAGGAGATCACAGCA 2128
Qy      578 ArgMetProGlyLysAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLys 597
Db      2129 ACAACTCTCGCGAGATACAGCTTACTTTGCTTCTGACAGTCTTTGCTTAAGATCGC 2188
Qy      598 AspTyrPheMetAsnThrAsnPheAlaLysTyrTyrAlaGlySerLeuArgLeuGlnHis 617
Db      2189 AATCATATTAACAGTAAAGAACCGAGATTAATCTTACGTCCTTTGATTTCCACCAT 2248
Qy      618 AspAlaSerLeuTyrSerValValSerIleLeuLeuGlyGlnGlyLysLeuArgGluIle 637
Db      2249 ACAAGAAAGGCTCTTGCACATCGCAATTCCTCTGGGAGAAACCAACCGAGCTCCCTGG 2308
Qy      638 LeuLeuProTyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGly 657
Db      2309 GTCCTCTCGAGATCTCCAGATCATCTCTTATGCTTGAATGCTTAATTCAGTTATTC 2368
Qy      658 HisThrAspHisLeuArgMetLysThrGlnSerLeuProProProProThrLeuSerThr 677
Db      2369 CATACAGAACACACATGAAG-----ACATATTTATACC 2401

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Qy 678 Asph1str-----SerTrpGlyGlyValThrAlaGlyGluLeuGlyThr 693
 Db 2402 GATACCTGATCATCAGAGGTTCTTGAGAAACAGATGCTTGTGACATCTTGACT 2461
 Qy 694 ArgValAlaValGluAsnThrSerGlyArgGlyPhePheGlnGlyThrProPheVal 713
 Db 2462 AGCCGCGCTTTGTT---ATTCCGCTCCGTTATCTTGAAAGAGTGAACCTTTGTC 2518
 Qy 714 LysValGlnAlaValThrAlaArgGlnAspSerPheValGluLeuGlyAlaIleSerArg 733
 Db 2519 AAAGACGATATATCTATGCGATCAGACAGACCTTACAGACCTGATGAGAGAGC 2578
 Qy 734 AspPheSerAspSerHisLeuValTrpAsnLeuAlaIleProLeuGlyIleLeuLeuGlyLys 753
 Db 2579 GCTTCAATTAAGAGAGCTTATCACTAGAGATCTTCAATAGGGTGACCTTGAAAGA 2638
 Qy 754 -----ArgPheAlaGluGlnThrTrpHisValAlaIleMetTyrSerProAspValCys 771
 Db 2639 GACTCAAAATCAGAAAGGAACTTACATCTTACTTATATATCTGATGCTTAC 2698
 Qy 772 ArgSerAsnProLysCysThrThrLeuLeuSerAsnGlnGlySerTrpLysThrLys 791
 Db 2699 CGACCGAATCTCAAAATGTCAACTTCCCTAATAGCTAGAGATGCTAAGTGAATGCGCTAT 2758
 Qy 792 GlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGly 811
 Db 2759 GGTACCAACTGCGACGACAGAGTTTCTGCTGCTGCGACCAACATTTCCAGATGAC 2818
 Qy 812 AlaAlaAlaGluLeuPheGlyAsnPheGlyPheGlnTrpArgGlySerSerArgSerTyr 831
 Db 2819 CCCCACTAGAAATCTTCGCTCAATTCGCTTGAAGTGAAGAAAGTTCTTCAAGAAATAT 2878
 Qy 832 AsnValAspAlaGlySerTyrIleLysPhe 841
 Db 2879 AATACAAACTAGGCTCTAAGTTTGTTC 2908

RESULT 14 US-10-324-129-1

; Sequence 1, Application US/10324129
 ; Publication No. US20030157124A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mardin et al.
 ; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses there
 ; FILE REFERENCE: 77613-4
 ; CURRENT APPLICATION NUMBER: US/10/324,129
 ; PRIOR FILING DATE: 2002-12-20
 ; PRIOR APPLICATION NUMBER: US 60/113,439
 ; PRIOR FILING DATE: 1998-12-01
 ; PRIOR APPLICATION NUMBER: US 60/132,272
 ; PRIOR FILING DATE: 1999-05-03
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1
 ; LENGTH: 3050
 ; TYPE: DNA
 ; ORGANISM: Chlamydia pneumoniae
 ; FEATURES:
 ; NAME/KEY: CDS
 ; LOCATION: (101)..(2908)
 ; US-10-324-129-1

Alignment Scores:

Pred. No.: 1,686-126 Length: 3050
 Score: 1335.50 Matches: 311
 Percent Similarity: 49.26% Conservative: 157
 Best Local Similarity: 32.74% Mismatches: 359
 Query Match: 31.09% Indels: 123
 DB: 13 Gaps: 14

US-09-830-446-27 (1-841) x US-10-324-129-1 (1-3050)

Qy 1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20

Db 101 ATGAAGTCCTGCTGCTGCTGCTGCTGCTTCTTCAATCCCGCTCTTTCATCCGCTCT 160
 Qy 21 LeuLeuGlyAlaIleThrThrGluGluLeuSerLaseAsnSerPheAspGlyThrThr 40
 Db 161 ATATGCGGCGAGAGGAGCTTAGAT--AGCGAATATATCTATGATGAGATCTAAC 217
 Qy 41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTrpValPhe 60
 Db 218 GGAATCACTTCAAGGCTTTTCCATACGAGACGCTGCTGAGAACTACTATTCCTTA 277
 Qy 61 LysAspSerValIleGluAsnValProLysThrGlyIleThrGlnSerThrSerCys 80
 Db 278 CTTTCCGAGTATCTTCAAAATGACAGGGCTTTAGAAATCCCTTACCTCAGATGTC 337
 Qy 81 PheLysAsnAspAlaAlaGlyAspLeuAsnPheLeuGlyGlyLysPheSerPheThr 100
 Db 338 TTCTAGAA-----GGGGGGGAGATCTTATCCAAAGGAAATCAACATGACTGAG 391
 Qy 101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsn 120
 Db 392 TTTCATTTATCATGCGGGCTGACGCTGAGACTGACGATCTGACGACGAT 451
 Qy 121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
 Db 452 AAGATCTTCTTAAATGATTTTCTAGACTCTATATCTCTTGCCCTCTTCTT 511
 Qy 141 ValThr--AsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAsn 159
 Db 512 CTCTCTCTACTGACATGCTTAAATCTGGGAAATCTATCTTAACTGACATGCGCAT 571
 Qy 160 AspLysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsn----- 177
 Db 572 TCCAAATATATTTACTCAGAACTTCTGTCATATAGCGGGTGTATATACGAAA 631
 Qy 177 ----- 177
 Db 632 AACTTTATATACGAGACATCTCACTTTCGAGCTTTTCGAGAAACAAGCTTCACA 691
 Qy 178 -----CysAlaGlySerLeuLysIleAlaAsn----- 186
 Db 692 GGAAGACAGGCGGTAGTTTACGTTACGTAAGAACTATATCTAGAAACAGCCCTGGG 751
 Qy 186 ----- 186
 Db 752 ATAGTTCTTCTCTCAAACTGACGAAGAGATCTGGCGTCTGTATACAGCATGAC 811
 Qy 186 ----- 186
 Db 812 AACTGTCATTACAGATACTTCAAGTATCTTTGACGGCAATAGCTTGGGAAGCC 871
 Qy 186 ----- 186
 Db 872 GCTCAAGCTCAGGGCGGCTATTGTTGCACTACGACAGATTAACAGTACTTACT 931
 Qy 187 ---AsnLysSerLeuSerPheIleGlyAsnSerSerThrArgGlyGlyAlaIleHis 205
 Db 932 GGGAAACAAACCTCTCTTTCACAAATATACAGATGACATATGGCGAGCATCTCT 991
 Qy 206 ThrLysAsnLeuThrLeuSerSerGlyGlyIleThrLeuPheGlnGlyAsnThrAlaPro 225
 Db 992 GGACTCAAGTCAGTATTTCCGCTGAGGTCCTACTCTATTTCAAGTAATATCTCAGA 1051
 Qy 226 ThrAlaAlaGlyLys-----GlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSer 243
 Db 1052 AGTACCGCGCTCAGGAGAGGAGGAGCGATCAATATAGATCTGCGGGAATCGCT 1111
 Qy 244 IleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAlaThrGlyThr 263
 Db 1112 CTCTCTGCTACTTTCGAGATATTACTTCAATACACCAAGTACCAACGAGAAAGACA 1171
 Qy 264 ValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAla 283

Db 1172 AGTACAGAAAGCGAATAATCATGATACCGTAAGTCATCGATACGAGCTGCT 1231
 Qy 284 GNGLYHLETHRIETHPHETRYRAPPRIETHTVALTHRGYSETHRSEVALA 303
 Db 1232 AGGGGCAATCTATCTATTTCTATGATCCATCAAAATCCAGAAACCGAGCTTCTACC 1291
 Qy 304 AAPALALEUANILEANSEPRORAPTHRGYASPAANLYSGIUTYTRQIYTHRIIE 323
 Db 1292 GACACATTGAACCTTAATCTTAGACAGATGCGAACGATGAGATGAGATGGGGGTGGGATT 1351
 Qy 324 VALPHSESGIYGLULYSEUTHRGUAGLUALALYEHAPOLULYBAENATHTHRSER 343
 Db 1352 GCTTTTTCGAGAAAGCTTTCCTCCATCAGAAAGCAATCCGTCGCAACCTGACCTCT 1411
 Qy 344 LYLEULEUGLINAVALALAPHELYBAENGLYTHRVATVALLEULYSGIYASPVALVAL 363
 Db 1412 ACTATCCGACACCTGCAATTAAGCGGGGAGATCTTGTACTTGATGAGAGTACC 1471
 Qy 364 LEUSERALAANGLYPHSESGIINAPALABANSETHLYSEULIEMETAPLEUGLYTHR 383
 Db 1472 GRTACTTTCAGAGATGATGATCAAGTCCAGATCCGATCTTAATGATGGGGGAGCT 1531
 Qy 384 SERLEUVALALABANTHRLGUSERLIEGLULEUTHRANLEUGLULEANILEAPSER 403
 Db 1532 ACACCTTAGTCTAAGAGCGCAATCTTTCGCTTAATGCTTACGACGTAATCTCTCCTCT 1591
 Qy 404 LEUARGANGLYLYSELYLEULEUSERALALATHRALAGLINSAPRIEARGYLE 423
 Db 1592 TTATGATGACCAACAGGAGCTTTTAAACAGAAAGCTGCAATTAATAATATCACTCA 1651
 Qy 424 ASPARGPROVALVALLEUALALIESEASPGIUSERPHERYRGINANGLYPHELEUAN 443
 Db 1652 TCGGAGAACATTCGCTATATGACAGGAAAGGTCAATTCATGATCAATCACTTAATAA 1711
 Qy 444 GLUAPHSISERTYRAPHOLYILEUGLULEU---ASPLAGLYYASAPRIEVALIIE 462
 Db 1712 AGTCTAGTACCTATCTCT---CTTCTTGAACTTAACCAACGAGAACCAACGAGAT 1768
 Qy 463 SERALASPSERARGSERILEAPALAVAGLINSERPRO-----TYRGLYTRGIN 479
 Db 1769 ACTCTGGAGAGCTTTTCTACCTGACTCTTCAGAAACCTGAACCACTACGGGTATCA 1828
 Qy 480 GLYLYSTPTHTRIEANTTP-----SETHRASAPLYSELYSALATHTVALISERTTP 497
 Db 1829 GGAACCTGCGAGATTCCTTGCGGAATGCAACATCTCAAAATATAGGAACCACTACG 1888
 Qy 498 ALALYSEGLISERPHESANPROTHRALAGLUNGILUALAProleuValProleuLeu 517
 Db 1889 ACCCGTACAGATACATCTCTAGTCTCGAGAAAGTAATCTCCTCTAATATAGCTTA 1948
 Qy 518 TTPGLYSEPHETIIEAPVALARGSERPHEGLINABNPHIELGLULEUGLYTHRGJUGLY 537
 Db 1949 TGGGAAACCTTATATATATATACGCTGATCAATCACTTATATACCAAGTCCAGTGG 2008
 Qy 538 ALAPROTYGLULYASRPHETPVALAAGLYLIESEZANVALIEUHSIARGSERGLY 557
 Db 2009 GAGCCTTTTGAAGGTAGCATGCTTTCAGGAATTCGCAATTTCTCTATAGAGATTC 2068
 Qy 558 ARGGLUANGILNARGLYSEPHARGHIEVALSERGLYVALAVALAGLYALASERTHR 577
 Db 2069 ATGCCACACCGCATGATTCCTCCCATATCAACGCGGGGTATATCACTGAGATCAACGA 2128
 Qy 578 ARGMEPRGGLYGLYAPRTHRIEUSERLEUGLYPHEALGLINEUPHEALAAARGAPLYS 597
 Db 2129 ACACTCTCGCCGAGATCAAGCTTACTTTCCTTTCGCGAGCTCTTGTATAGATTCG 2188
 Qy 598 ASPTYRPHMETANRANRANPHEALALYETHRTYRALAGLYSERLEUARGLEUGLINHS 617
 Db 2189 AATCATATTAACAGTAAAGCAACGAGATCTTAAGGTGCTCTTGTATTTCCACCAT 2248
 Qy 618 AAPALASERLEUTYRSEVALVALSERILEULEUGLYGLULYGLYLEUARGJULIE 637
 Db 2249 ACAGAGGCTCTTCGACATCGCAATTCCTCTCGGGGAAACCAACCGAGCTCCTCG 2308

Qy 638 LEULEUPROTYRVALSERIETHRIEUPROCYSESPHERYGLYGLINEUSERTYRGLY 657
 Db 2309 GTGCTCTCGAGATCTCCAGATCAATCTCTTATGCTTATGATGATGATGATGATGAT 2368
 Qy 658 HLETHRASPHIARNGELYSETHRGUSELEUPROPROBROTHRIEUSERTHR 677
 Db 2369 CATACAGAACACCATGAAG-----ACATATATATATATATATATATATATATATAT 2401
 Qy 678 AAPHLETH-----SETPRGLYGLYTRVALITPRALAGLYLEUGLYTHR 693
 Db 2402 GATATCTATCATCAAGGCTCTTGAGAAACGATGCTTCTGAGCAATCTTGAGAGCT 2461
 Qy 694 ARGVALALVALIGLUBANTHRSERGLYARGGLYPHEPHEGLINGLUTYRTHRPROPEVAL 713
 Db 2462 AGCCTCCCTTTGTT---ATTTCCTCCGTATCTTCTGAAAGAGTCAACCTTTTGTG 2518
 Qy 714 LYSEVALGINALVALATYRALAARGIINAPSERPHEVALIGLULEUGLYALALIESEARG 733
 Db 2519 AAAGTACATATATATATATGCGATGAGCAAGCTTCTACGAGGCTATGCTGAAGAGCC 2578
 Qy 734 AAPHSESERAPSERHILEUTYRANLEUALALIEPROLEUGLYLYLEULEUGLYS 753
 Db 2579 GCTTCAATMAAGCGAGCTTATCAAGTACGATTCCTATGAGGCTCACTTCGAAAGA 2638
 Qy 754 -----ARGPHEALAGLULINTYRTHIIEVALALAMETYSERPROASPVALCY 771
 Db 2639 GACTCAAAATCGAAGAAAGGAACTTACATCTTACTTATATATATATATATATATAT 2698
 Qy 772 ARGSEANPROLYSEYETHRTHRIEULEUSERANGLIYSETRIPYSTRHS 791
 Db 2699 CGACGCAATCTTAATATGTCMAAATTCCTTAATAGTAGAGATGCTATGAGTGGCTAT 2758
 Qy 792 GLYSEANLEUALAARGIINALAGLYLEVALGINALASERGLYPHEARGSERLEUGLY 811
 Db 2759 GGTACCAACCTGCGACGACAGAGTTTCTGTTGCGTCCGACCAACCATTTCCAAAGTAA 2818
 Qy 812 ALALALAGLULEUPHEGLYANPHEGLYPHEGLUTPRARGLYSERSEARGSERTYR 831
 Db 2819 CCCCATGAAATCTTCGATCAATTCGCTTTGAGATGAGATGAGATTTCTCAAGAAATAT 2878
 Qy 832 AENVALASPALAGLYSERLYSELYSPHE 841
 Db 2879 AATACAAACCTAGGCTCTAAGTTTGTTC 2908

RESULT 15
 US-09-738-269-56
 ; Sequence 56, Application US/09738269
 ; Publication No. US20030185848A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHNSTON, STEPHEN A.
 ; APPLICANT: STEKE-HALE, KATHERINE
 ; APPLICANT: SYKES, KATHRYN F.
 ; APPLICANT: KALTENBOCK, BERNHARD
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
 ; TITLE OF INVENTION: NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
 ; TITLE OF INVENTION: CHLAMYDIA PSITRACI
 ; FILE REFERENCE: US/09-738,269
 ; CURRENT APPLICATION NUMBER: US/09/738,269
 ; CURRENT FILING DATE: 2000-12-18
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 56
 ; LENGTH: 2781
 ; TYPE: DNA
 ; ORGANISM: Chlamydia psitraci
 US-09-738-269-56

Alignment Scores:
 Pred. No.: 1,586-121 Length: 2781
 Score: 1286.50 Matches: 327
 Percent Similarity: 47.49% Conservative: 127
 Best Local Similarity: 34.21% Mismatches: 357

Query Match: 29.95% Indels: 145
DB: 13 Gaps: 17

US-09-830-446-27 (1-841) x US-09-738-269-56 (1-2781)

Qy 1 MetIysIlePheLeuAsgPheLeuIleSerLeuValProThrLeuSerMetSer--- 19
Db 1 ATGAGGCGCTCTTATATATAGATTTTATATCTGTGACGCTGACCTTACCAATATCTTTT 60
Qy 20 -----AsnLeuLeuIValIaIaIaThrThrGluGluLeuSerIleSerAsn 34
Db 61 CACTTCGCAATGCAATGCAAGAGTGGCTTTAACTCAAGAAATCTATCTCGATGCAAT 120
Qy 35 SerPheAsgIlyThrThrThrThrThrThrThrThrThrThrThrThrThrThr 54
Db 121 GGA-----GCAATTCAGCTCGCAATCTACAGAGCAGCGCGG 156
Qy 55 G1yThrAsnIyValPheLeuAsgPheValIleGluAsnValProLeuThrGlyGlu 74
Db 157 GGAACGATTTCACAGCTGAGAGTGTATTTCTATGTAGATGTAGAGCAGACGCGCT 216
Qy 75 ThrGlnSerThrSerCysPheLeuAsgAAsnIaIaIaIaGlyAAsnLeuAAsnPheLeuGly 94
Db 217 CTGGCTTCTCAAGCTTTTGTTCAG-----ACTGCAAGACACTTAACTTTCAAGG 267
Qy 95 G1yGlyPheSerPheThrPheSerAsnIleAAsnIaIaIaThrIleAAsnGlyValIaIaIle 114
Db 268 AACACACATAGCTTATCCATACAGAACGCAATGCC---GGAGCAATCTCGCGGGAAT 324
Qy 115 G1ySerGluIaIaIaAsnIyThrValIleThrLeuSerGlyPheSerIleLeuSerPheLeu 134
Db 325 AACGTTAACCTGCGCATAGATGATCTTACGCTGACAGATTTTCTTAAGTTGAGCTTTTAA 384
Qy 135 LysSerProIleSerThrValIleThrAsnGlyLeuGlyIaIeAsnValIyGlyAAsnLeu 154
Db 385 GAATGCCCATCTCTCTAGTGAATCTGGAAGAGGCGATGAAATCCGAGAGACATTA 444
Qy 155 SerLeuAAsnAAsnAAsnIyValIleuIleGlnAAsnAAsnPheSerThrGlyAAsnIyGly 174
Db 445 AACCTAAGGAATATAGCCAGATTTCTGTGTATCAGAACTATTCGCGTGAAGATGTGGA 504
Qy 175 AlaIleAsnCys----- 178
Db 505 GCCATCTCTGCAAGCTTTTCTCTAAACGCGCTGAGCAAGAAATGACTTCACCACT 564
Qy 178 ----- 178
Db 565 AACTCTACTGCAAAAAAGTGGAGCGAGTCTGCTAGCGGAATAGCTCATTTCGAGC 624
Qy 178 ----- 178
Db 625 AACCAAGGACAAATGAGATTTCTGGGAACACTGCTGTGAATTCGGGGAGACATATAT 684
Qy 178 ----- 178
Db 685 TCAGAGCTTCTATGACGATTCGAGTAAACAACAGTTGCTTTTGAACAACATCTGTT 744
Qy 179 -----AlaGly 180
Db 745 TCCGCTTACTGATGCTTGGCGGTGAGCTATCTGTAGCAAAAAGGTTCAACACCG 804
Qy 181 SerLeuIyIleIaIaAsnAAsnIySerLeuSerPheIleGlyAAsnSerSerThrArg 200
Db 805 ACCCTTACTATAGAGATACAAAGCTTGAATTTTGAAGAAATACCTTCTTCAGCAAAA 864
Qy 201 G1yGlyIaIaIeIleThrIyAAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220
Db 865 GGTGAGGAGATTACACCGATTAACATATGACTTGTGGGCGCTTACCGCATTTATC 924
Qy 221 GlyAsnThrIaIaProThrIaIaIaGlyGlyGlyIaIaIaIaIleIaIaAAsnSerGly 240
Db 925 AATAACAAAGTTAACCAATGCTACACCTAAGGGTGAAGTATGTGATGCTGCACATGGA 984

Qy 241 ThrLeuSerIleSerGlyAAsnSerGlyAAsnIleIlePheGluGlyAAsnThrIleGlyIaIa 260
Db 985 GAATGATGCTTAACCGCTGCAACATGAGGATATCTTTGATATATACCTGATGCCACA 1044
Qy 261 -----ThrGlyThrValSerHisSerIaIleAAsnLeuGlyThrSerIaIaIyIleThr 278
Db 1045 CAGACCAATGCTAACAATTAAGAAAGAAATGCAATTAACATTAAGCAATGTAATTTGCTC 1104
Qy 279 AlaLeuArgIaIaIaGlnGlyIleThrIleThrIyPheIyAAsnProIleThrValThrGly 298
Db 1105 AACTTACGTGAGCGTCTGGAAGAACAGATTTCTTATATATCTTATCAGCTTGAAAGT 1164
Qy 299 SerThrSerValIaAAsnIaIeAAsnIleAAsnSerProAAsnThrGlyAAsnIyGly 318
Db 1165 -----AATGCTGCTGATCTTCTCACTTGAATTAAGCTGAG---GGTGAAT---AAAACG 1212
Qy 319 TyrThrGlyThrIleValPheSerGlyGluIyLeuThrGluIaIaGluIaIaIyAAsnGly 338
Db 1213 TATATGGAAGATTAATTTTTCAGAGAAAGCTCACTGAAGAACAGCTGCTGTTGCG 1272
Qy 339 LysAAsnArgThrSerIySLeuLeuGlnAAsnValaIaPheLysAAsnGlyThrValIleu 358
Db 1273 GATAACCTTAAGACACATTTACACAGCCTATCACTTACGCTGCTGGAATCTTGTTA 1332
Qy 359 LysGlyAAsnValIleuSerIaIaAsnGlyPheSerGlnAAsnIaAAsnSerIyLeuIle 378
Db 1333 CGCAGCGGTGGGAATGAAGAAACAAACAGCTCGCAACACAGCAGATCTTTGATCTG 1392
Qy 379 MetAAsnLeuGlyThrSerLeuValaIaAsnThrGluSerIleGluLeuThrAAsnLeuGlu 398
Db 1393 ATGATGACAGGACAAAGTTATCCGCAAAAACAAAGATGCTTACATGACCAATCTGCT 1452
Qy 399 IleAAsnIleAAsnSerLeuAAsnGlyLysIySLeuSerIaIaIaThrIaIaGln 418
Db 1453 ATTAATCCGAATACTTATGATGGAAGAAATATCCCGATGATGATCCGCTGCTGCTG 1512
Qy 419 LysAAsnIleArgIleAAsnArgProValIaIeIaIaIleSerAAsnGlySerPheIyGln 438
Db 1513 AAGATGATGCTTATATGACGGGTATGCGCTATGATGCTTACAGAGCAAGCTTTATGAA 1572
Qy 439 AsnGlyPheLeuAAsnGluAAsnIleSerIyAAsnIyIleLeuGluLeuAAsnIaIaGlyLys 458
Db 1573 AACCATTAAGCTTAATGATACCTTATGAGAGAAATCAACTTTTCGGGAAGGTTGCG 1632
Qy 459 AAsnIleValIleSerIaIaAAsnArgSerIleAAsnIaIaGlnSerProIyGlyTyr 478
Db 1633 GTGACACACACACACGCGCCATGATCATGCTGTGTGTGTGTGTGAACCATATGTTAT 1692
Qy 479 GlnGlyLysIyThrIleAAsnIySerThrAAsn-----LysLys 492
Db 1693 CAAGGAACCTGCTGTCAGTGGGTCAAGATATATACCTGATCTTAACCAACAAACA 1752
Qy 493 AlaThrValSerIyPheIyGlnSerPheAsnProThrIaIaGluGlnIaIaIaProLeu 512
Db 1753 GCAATCTTTACTGAAATTAACAGATATGTTCCAATCTGAACGCTGCTCGCTGA 1812
Qy 513 ValProAAsnLeuLeuIyPheIySerPheIleAAsnValArgSerPheGlnAAsnIleGlu 532
Db 1813 GTACTCAATACCTTTGGGAGATCCTTATATAGATTTAGCTTATTAACAAGTCTTGGA 1872
Qy 533 LeuGlyThrGluGlyIaIaProIyGluIyAAsnArg---PheThrValaIaGlyIleSerAsn 551
Db 1873 CGTAGTGTGATGATATCTTGAAGACAGCTGTGTGTGTGTGTGTGGAATGGGAAC 1932
Qy 552 ValLeuHisArgSerGlyAAsnGluAAsnIaIaArgIySLeuAAsnIyIleValSerGlyIaIa 571
Db 1933 TTCTTCATTAAGATCGGAATGCTGAANAATGCAAAATTCGCTCATATCAGTTGGGAAT 1992
Qy 572 ValIaIaGlyAAsnIyArgMetProGlyIyAAsnThrLeuSerLeuGlyPheIaIaGln 591
Db 1993 GTGTTAGAGCCACAAACAAATACCTCGAGAGAGATTTCTTATGTGTGCTTCTGTCAG 2052
Qy 592 LeuPheIaIaArgAAsnIyAAsnIyPheMetAAsnThrAAsnPheIaIaIyThrIaIaGly 611

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: January 29, 2004, 10:21:11 ; Search time 7888 Seconds
(without alignments)
4361.688 Million cell updates/sec

Title: US-09-830-446-27

Perfect score: 4295
Sequence: 1 MKIPRFLIBLVPTLSMSN.....FEMRGSSRSYNDAGSKIKF 841

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 segs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODX=frame+ p2n model -DRV=rjh
-Q=/cgn2.1/USFTO.spool/US09830446/runat.29012004.102102.19204/app.query.fasta.1.1031
-DB=GenEmbl -Qfmt=fastap -SUFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pcpt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=PCPT -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09830446 @CCN 1.1.5272 @runat.29012004.102102.19204 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEBUFRY -NEG_SCORES=0 -WAIT -DSFLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl :
1: gb_ba :
2: gb_hcg :
3: gb_in :
4: gb_cm :
5: gb_ov :
6: gb_pac :
7: gb_ph :
8: gb_pl :
9: gb_pr :
10: gb_ro :
11: gb_sbs :
12: gb_ey :
13: gb_un :
14: gb_vl :
15: em_ba :
16: em_fun :
17: em_hum :
18: em_in :
19: em_mu :
20: em_or :
21: em_ov :
22: em_pac :
23: em_ph :
24: em_pl :
25: em_pi :
26: em_ro :
27: em_sbs :
28: em_un :

29: em_vl :
30: em_hcg_hum :
31: em_hcg_inv :
32: em_hcg_other :
33: em_hcg_mus :
34: em_hcg_pln :
35: em_hcg_fod :
36: em_hcg_mam :
37: em_hcg_vrt :
38: em_ay :
39: em_hgo_hum :
40: em_hgo_mus :
41: em_hgo_other :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4295	100.0	2526	6 AX349617	AX349617 Sequence
2	4295	100.0	10574	1 AE001586	AE001586 Chlamydia
3	4295	100.0	12127	1 AE002235	AE002235 Chlamydia
4	4295	100.0	26920	1 CPN133035	AJ133035 Chlamydia
5	4278	99.6	2526	6 AB1833	AB1833 Sequence 7
6	4260	99.2	299650	1 AP002545	AP002545 Chlamydia
7	4255	99.1	110000	6 AR310754_00	AR310754 Sequence 29
8	2603	60.6	1830	6 AB1855	AB1855 Sequence 9
9	1569.5	36.5	2787	6 AB1835	AB1835 Sequence 9
10	1558.5	36.3	16448	1 AE001587	AE001587 Chlamydia
11	1497	34.9	2520	6 AX662085	AX662085 Sequence
12	1487	34.9	2520	6 AX662157	AX662157 Sequence
13	1487	34.9	6110	1 CP065942	U65942 Chlamydia
14	1487	34.9	6234	1 CP065943	U65943 Chlamydia
15	1435.5	33.4	2787	6 AX349593	AX349593 Sequence
16	1435.5	33.4	3200	6 AB1827	AB1827 Sequence 1
17	1435.5	33.4	6030	1 CP0654	AJ001331 Chlamydia
18	1435.5	33.4	10757	1 AE001628	AE001628 Chlamydia
19	1435.5	33.4	12676	1 AE002192	AE002192 Chlamydia
20	1435.5	33.4	17280	1 CPN133034	AJ133034 Chlamydia
21	1435.5	33.4	110000	6 AR310754_05	Continuation (6 of
22	1435.5	33.4	30650	1 AP002546	AP002546 Chlamydia
23	1415.5	33.0	2793	6 AX349523	AX349523 Sequence
24	1415.5	33.0	10026	1 AE002193	AE002193 Chlamydia
25	1415.5	33.0	15068	1 AE001627	AE001627 Chlamydia
26	1407.5	32.8	2787	6 AX349573	AX349573 Sequence
27	1406.5	32.7	2793	6 AB1841	AB1841 Sequence 15
28	1406.5	32.7	2815	6 AB1829	AB1829 Sequence 3
29	1406.5	32.7	12676	1 AE002192	AE002192 Chlamydia
30	1406.5	32.7	17280	1 CPN133034	AJ133034 Chlamydia
31	1406.5	32.7	30650	1 AP002546	AP002546 Chlamydia
32	1402.5	32.7	2757	6 AB1837	AB1837 Sequence 11
33	1396	32.5	300955	1 AE016996	AE016996 Chlamydia
34	1390	32.4	10757	1 AE001628	AE001628 Chlamydia
35	1379.5	32.1	2787	6 AX349511	AX349511 Sequence
36	1377.5	32.1	2787	6 AB1839	AB1839 Sequence 13
37	1366.5	31.8	300512	1 AE016995	AE016995 Chlamydia
38	1365	31.8	110000	6 AR310754_05	Continuation (6 of
39	1359.5	31.7	3000	6 AB1851	AB1851 Sequence 25
40	1359.5	31.7	6030	1 CP0654	AJ001331 Chlamydia
41	1357.5	31.6	2241	6 AX349497	AX349497 Sequence
42	1335.5	31.1	2811	6 AX349631	AX349631 Sequence
43	1311.5	30.5	110000	6 AR310754_04	Continuation (5 of
44	1286.5	30.0	2781	6 AX662119	AX662119 Sequence
45	1286.5	30.0	2781	6 AX666191	AX666191 Sequence

RESULT 1

ALIGNMENTS

AX349617 LOCUS AX349617 2526 bp DNA linear PAT 06-FEB-2002
 DEFINITION AX349617 140 from Patent WO202606.
 ACCESSION AX349617 GI:18615415
 VERSION AX349617.1 GI:18615415
 KEYWORDS Chlamydia pneumoniae
 SOURCE Chlamydia pneumoniae
 ORGANISM Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 REFERENCE 1 Ratti, G. and Grandi, G.
 AUTHORS Immunisation against Chlamydia pneumoniae
 TITLE Patent: WO 0202606-A 140 10-JAN-2002;
 JOURNAL Chiron S.P.A. (IT)
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 BASE COUNT 693 a 493 c 601 g 739 t
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 Score: 4295.00 Matches: 841
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-830-446-27 (1-841) x AX349617 (1-2526)

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RESULT 2
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 ACCESSION AB001586 AB001363
 VERSION AB001586.1 GI:4376263
 KEYWORDS
 SOURCE Chlamydia pneumoniae CWL029
 ORGANISM Chlamydia pneumoniae CWL029
 Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 REFERENCES
 1 (bases 1 to 10574)
 Kaiman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Hyman, R.W.,
 Olinger, L., Grimwood, J., Davis, R.W. and Stephens, R.S.
 Comparative genomes of Chlamydia pneumoniae and C. trachomatis
 Nat. Genet. 21 (4), 385-389 (1999)

MEDLINE 99206606
 PUBMED 10192388
 REFERENCE 2 (bases 1 to 10574)
 AUTHORS Kaiman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Olinger, L.,
 Grimwood, J., Davis, R.W. and Stephens, R.S.
 TITLE Direct Submission
 JOURNAL Submitted (01-DEC-1998) Program in Infectious Diseases, University
 of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA
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BASE COUNT 3217 a 1747 c 2651 g 2959 t

Alignment Scores:

Pred. No.: 7,13e-255 Length: 10574
Score: 4295.00 Matches: 841
Percent Similarity: 100.00% Conservative: 0
Beet Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 1

US-09-830-446-27 (1-841) x AE001586 (1-10574)

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BASE COUNT 3532 a 2722 c 2431 g 3441 t 1 others

ORIGIN

Alignment Scores:

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Query Match: 1	Gaps: 0	841	0	0	0

US-09-830-446-27 (1-841) x AB002235 (1-12127)

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 REFERENCES
 1. Daugaard, L., Hjerno, K., Knudsen, K., Madsen, A.S., Christiansen, G. and Birkeland, S.
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 JOURNAL
 Boesen, T.
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 AUTHORS Maden, A. and Birkelund, S.
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 AUTHORS Shirai,M., Hirakawa,H., Ouchi,K., Tabuchi,M., Kishi,F., Kimoto,M., Takeuchi,A., Nishida,J., Shibata,K., Fujisaga,R., Yoneda,H., Matsushima,H., Tanaka,C., Furukawa,S., Miura,K., Nakazawa,A., Ishii,K., Shiba,T., Hattori,M., Kuhara,S. and Nakazawa,T.
 TITLE Comparison of outer membrane protein genes omp and pmp in the whole genome sequences of Chlamydia pneumoniae isolates from Japan and the United States
 JOURNAL J. Infect. Dis. 181 Suppl 3, S524-S527 (2000)
 MEDLINE 20298986
 PUBMED 10839753
 REFERENCE
 AUTHORS Shirai,M.
 TITLE Direct Submision
 JOURNAL Submitted (04-JUL-2000) Mutsunori Shirai, Yamaguchi University School of Medicine, Department of Microbiology, 1-1-1 Minamikogushi, Ube, Yamaguchi 755-8505, Japan (E-mail:shirai@po.cc.yamaguchi-u.ac.jp, Tel:81-836-22-2227, Fax:81-836-22-2415)
 COMMENT On or before Aug 31, 2000 this sequence version replaced gi:6172286, gi:6172288, gi:6172310, gi:6172312, gi:6172314, gi:6172316, gi:6172318, gi:6172320, gi:6172322, gi:6172324, gi:6635158, gi:6635160, gi:6635162, gi:6635164, gi:6635166, gi:6635168, gi:6635170, gi:6635172, gi:8547422, gi:8547426,

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ACCESSION AR310754
VERSION AR310754.1 GI:31704180
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

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REFERENCE 1 (bases 1 to 1230025)
AUTHORS Griffiths,R., Hoiseh,S.K., Zagursky,R.J., Metcalfe,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polymucleotides and uses thereof
JOURNAL Patent: US 6559294-A 1 06-MAY-2003;
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 AUTHORS Madsen, A. and BirkeLund, S.
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ACCESSION  AE001587
VERSION     AE001587.1
KEYWORDS   GI:4376271
ORGANISM   Chlamydia pneumoniae CML029
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REFERENCE  1 (bases 1 to 16448)
            Kalman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Hyman, R. W.,
            Olinger, L., Grimwood, J., Davis, R. W. and Stephens, R.S.
            Comparative genomes of Chlamydia pneumoniae and C. trachomatis
            Nat. Genet. 21 (4), 385-389 (1999)
TITLE      JOURNAL
MEDLINS    99206606
PUBMED     10192388
REFERENCE  2 (bases 1 to 16448)
            Kalman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Olinger, L.,
            Grimwood, J., Davis, R. W. and Stephens, R. S.
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TITLE      JOURNAL
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DEFINITION Sequence 22 from Patent WO02053588.
ACCESSION  AX662085
VERSION     AX662085.1  GI:29163040
KEYWORDS
SOURCE
ORGANISM    Chlamydomophila peitraci
             Bacteria; Chlamydiales; Chlamydiales; Chlamydiaceae; Chlamydomophila.
REFERENCE   1
AUTHORS     Johnston,S.A., Stenke-Hale,K., Sykes,K.F. and Kaltenboeck,B.
TITLE        Methods and compositions for vaccination comprising nucleic acid
             and/or polypeptide sequences for chlamydia peitraci
JOURNAL      Patent: WO 02053588-A 22 11-JUL-2002;
             BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
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QY      406      AsnGly-----LysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArg 422
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Qy      501 SerPheAapProThrAlaGlnGluAlaProLeuValProApuLeuLeuTrpGlySer 520
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DEFINITION Sequence 22 from Patent WO247718.
ACCESSION  AX666157
VERSION     AX666157.1 GI:29290977
KEYWORDS
SOURCE
ORGANISM   Chlamydomonas patitaci
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomonadales.
REFERENCE
1          Johnston, S.A.
            Methods and compositions for vaccination comprising nucleic acid
            ad/or polypeptide sequences of 1(chlamydia)
            Patent: WO 0247718-A 22-20-JUN-2002.
            BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)

FEATURES
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 VERSION U65942.1 GI:1617505
 KEYWORDS Chlamydia abortus
 SOURCE Chlamydia abortus
 ORGANISM Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 REFERENCE 1 (sites)
 AUTHORS Longbottom, D., Russell, M., Jones, G.E., Iainson, F.A. and
 Herring, A.J.
 TITLE Identification of a multigene family coding for the 90 kDa proteins
 of the ovine abortion subtype of Chlamydia psittaci
 JOURNAL FEMS Microbiol. Lett. 142 (2-3), 277-281 (1996)
 MEDLINE 96406378
 PUBMED 8810511
 REFERENCE 2 (sites)
 AUTHORS Longbottom, D., Russell, M., Dunbar, S.M., Jones, G.E. and Herring, A.J.
 TITLE Molecular cloning and characterization of the genes coding for the
 highly immunogenic cluster of 90-kilodalton envelope proteins from
 the Chlamydia psittaci subtype that causes abortion in sheep
 infect. Immun. 66 (4), 1317-1324 (1996)
 JOURNAL 9529048
 PUBMED 8810511
 REFERENCE 3 (bases 1 to 6110)
 AUTHORS Longbottom, D.
 TITLE Direct Submission
 JOURNAL Submitted (02-AUG-1996) Moredun Research Institute, International
 Research Centre, Pentlands Science Park, Bush Loan, Pentlands,
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 Percent Similarity: 56.21% Conservative: 132
 Best Local Similarity: 41.03% Mismatches: 321
 Query Match: 34.85% Indels: 60
 DB: 1 Gaps: 25

US-09-830-446-27 (1-841) x CP065942 (1-6110)
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 DB 2805 TCTTGAAGCTTCGTAACGACGCTCAAAAGCCTTAACCTCCGATAGCTATATGGA 2864
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 QY 139 SerThrValThrAsnGlyLeuGlyAlaIleAsnValIleGlyAsnLeuSerLeuAsp 158
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Qy      757 GluGln-----TyrTyrHisValValAlaMetCysTyrSerProAspValCysArgSer 773
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Qy      792 GlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGly 811
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Qy      812 AAlaAlaLeuLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArgSerTyr 831
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RESULT 14
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DEFINITION Chlamydomophila abortus clone S21 POMP91B precursor and POMP90B precursor, genes, complete cds.
VERSION   U659943
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ORGANISM   Chlamydomophila abortus
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AUTHORS    Longbottom,D., Russell,M., Jones,G.E., Lainson,F.A. and Herring,A.J.
TITLE      Identification of a multigene family coding for the 90 kDa proteinase of the ovine abortion subtype of Chlamydia psittaci
JOURNAL    JOURNAL OF CLINICAL MICROBIOLOGY
MEDLINE    96406378
PUBMED     8810511
REFERENCE   2 (sites)
AUTHORS    Longbottom,D., Russell,M., Dunbar,S.M., Jones,G.E. and Herring,A.J.
TITLE      Molecular cloning and characterization of the genes coding for the highly immunogenic cluster of 90-kilodalton envelope proteins from the Chlamydia psittaci subtype that causes abortion in sheep
JOURNAL    Interc. Immun.
MEDLINE    98187897
PUBMED     9529048
REFERENCE   3 (bases 1 to 6234)
AUTHORS    Longbottom,D.
TITLE      Direct Submission
JOURNAL    Submitted (02-AUG-1996) Moreduin Research Institute, International Research Centre, Pentlands Science Park, Bush Loan, Pentkirk, Midlothian EH26 0PZ, UK
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Pred. No.:	1.06e-82	Length:	6234
Score:	1497.00	Matches:	357
Percent Similarity:	56.21%	Conservative:	132

US-09-830-446-27 (1-841) X CPU65943 (1-6234)

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AUTHORS       Ratcl,G. and Grandt.G.  
TITLE         Immunisation against Chlamydia pneumoniae  
JOURNAL       Patent: WO 020606-A 116 10-JAN-2002;  
  
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US-09-830-446-27 (1-841) X AX349593 (1-2787)

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Db		118 GATTCAGGAACGGTTACTCCAAAACCTTCAGCC-----ACAACATATCTCTTA	165
OY		61 LybAspSerValIalIleGIuAsnValIProLystrhrglyIuThrGlserThrSerCyS	80
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OY		141 ValIthraNGlyLeuGIyAlaIleAsnValIySGlyAsnLeuSerLeuAspAsnaSp	160
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Copyright (c) 1993 - 2004 CompuGen Ltd.

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Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1365	31.8	1230025	4	US-09-198-452A-1
3	939	21.9	3021	4	US-09-556-877-182
4	939	21.9	3021	4	US-09-556-877-182
5	939	21.9	3021	4	US-09-556-877-182
6	936	21.8	2949	4	US-09-556-877-170
7	936	21.8	2949	4	US-09-556-877-170
8	936	21.8	2949	4	US-09-556-877-170
9	711.5	16.6	2643	4	US-09-556-877-169
10	711.5	16.6	2643	4	US-09-556-877-169
11	711.5	16.6	2643	4	US-09-556-877-169
12	696.5	16.2	2601	4	US-09-556-877-181

13	696.5	16.2	2601	4	US-09-620-412C-181	Sequence 181, App
14	696.5	16.2	2601	4	US-09-598-419-181	Sequence 181, App
15	527.5	12.3	2895	4	US-09-556-877-171	Sequence 171, App
16	527.5	12.3	2895	4	US-09-620-412C-171	Sequence 171, App
17	527.5	12.3	2895	4	US-09-556-877-171	Sequence 171, App
18	527.5	12.3	2895	4	US-09-556-877-183	Sequence 183, App
19	527.5	12.3	2895	4	US-09-620-412C-183	Sequence 183, App
20	527.5	12.3	2895	4	US-09-556-877-174	Sequence 174, App
21	506	11.8	5265	4	US-09-620-412C-174	Sequence 174, App
22	506	11.8	5265	4	US-09-556-877-174	Sequence 174, App
23	506	11.8	5265	4	US-09-556-877-173	Sequence 173, App
24	447.5	10.4	5331	4	US-09-620-412C-173	Sequence 173, App
25	447.5	10.4	5331	4	US-09-556-877-173	Sequence 173, App
26	447.5	10.4	5331	4	US-09-556-877-172	Sequence 172, App
27	433	10.1	4593	4	US-09-620-412C-172	Sequence 172, App
28	433	10.1	4593	4	US-09-556-877-172	Sequence 172, App
29	433	10.1	4593	4	US-09-556-877-184	Sequence 184, App
30	430.5	10.0	2547	4	US-09-620-412C-184	Sequence 184, App
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33	421	9.8	2847	4	US-09-620-412C-186	Sequence 186, App
34	421	9.8	2847	4	US-09-598-419-186	Sequence 186, App
35	421	9.8	2847	4	US-09-620-412C-344	Sequence 344, App
36	341	7.9	2103	4	US-09-598-419-344	Sequence 344, App
37	341	7.9	2103	4	US-09-620-412C-312	Sequence 312, App
38	333	7.8	2076	4	US-09-598-419-312	Sequence 312, App
39	333	7.8	2076	4	US-09-620-412C-328	Sequence 328, App
40	290	6.8	2148	4	US-09-598-419-328	Sequence 328, App
41	290	6.8	2148	4	US-09-620-412C-340	Sequence 340, App
42	266	6.2	1965	4	US-09-598-419-340	Sequence 340, App
43	266	6.2	1965	4	US-09-620-412C-356	Sequence 356, App
44	266	6.2	1965	4	US-09-598-419-356	Sequence 356, App
45	266	6.2	2052	4	US-09-598-419-356	Sequence 356, App

ALIGNMENTS

RESULT 1
US-09-198-452A-1
Sequence 1, Application US/09198452A
Patent No. 6559294
GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1
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 DB 29010 TTATATAGAGCTGCTACTACCAAGAGTATCGGCTAGCAATAGCTTGATGGAAGTCA 29069
 QY 41 SerThrThrSerPheSerSerIysThrSerSerAlaThrAspGlyThrAsnTyValPhe 60
 DB 29070 TCACAAACAAGCTTTTCTAGTAAACATCATCGGCTACAGATGAGCAACCAATATATGTTT 29129
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 DB 29250 TTTACCAATATCGATGCAACCAACGCTTCTGAGGCTGATGGAAGTCAACACACTAAT 29309
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RESULT 2

US-09-198-452A-1/c

Sequence 1, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffiths, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: Therect and uses thereof, in particular for the diagnosis, prevention

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 1

LENGTH: 1230025

Jan 30

OTR

ORGANISM: Chlamydia pneumoniae
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